

110682

Schreiber, David

From: Ramirez, Delia
Sent: Wednesday, December 17, 2003 10:38 AM
To: Schreiber, David
Subject: case 09/879792

Hi,

I would like to order the following interference search: seq id 11 and 12 in the nucleic acid databases.

Thank you,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
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Arlington, VA 22202
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Db 61 TCGAGCATCTCCAGCCACAGGCATCTCCAGCTGGGACACCTCCAGGCGCGGCATCTCCAGC 120
Qy 121 CCAGGCATCTCCAGCCACAGGCATCTCCAGCTGGGACACCTCCAGGCGCGGCATCTCCAGC 180
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Qy 181 CCAGGCATCTCCAGCTGGTACACTCCAGGCGCGGCATCTCCAGGCGCGGCATCTCCAGC 240
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Qy 241 CCAGGCATCTCCAGGCGCGGCATCTCCAGGCTGGGATCACTCTCCAGGCTCCATCCCGG 300
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Qy 301 CAGGTCATCATCCGCCAGGCTCAGGCTGGGATCACTCTCCAGGCTCCATCCCGG 360
Db 301 CAGGTCATCATCCGCCAGGCTCAGGCTGGGATCACTCTCCAGGCTCCATCCCGG 360
Qy 361 TAGAGCAACCAAGTGGGCTGTACCCATCCGATCACTCTCCAGGCTCAGGCTCAGGCT 420
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Qy 421 AACAGGCGCACAGGAGGAGCCAGGTACAGGCTGCCCAAGTTCACTCTGGCGGAGGG 480
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Qy 541 CATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
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Qy 1201 CAAACGCAATTACACCGATGAGGAGGACGACTATATGACATCGCCCTCATATGGGCTGTCCAA 1260
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Qy 1381 GACATCCCCCTTCTCTCGGAGGCTGAGGTCATATCTCATCTCTCAAGAAATGCAATGA 1440
Db 1381 GACATCCCCCTTCTCTCGGAGGCTGAGGTCATATCTCATCTCTCAAGAAATGCAATGA 1440
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Db 1681 GCGATTCAGAAAATCTTAACAGCTGGCTGTCTCTGACAGCAGCAGGCTGTCTGTGAC 1740
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Db 1741 TCGAGAAA 1748

RESULT 2

US-10-353-690-99

; Sequence 99, Application US/10353690

; Publication No. US20030215840A1

; GENERAL INFORMATION:

; APPLICANT: Logan, Thomas Joseph

; APPLICANT: Chun, Miyoung

; APPLICANT: Galvin, Katherine M.

; APPLICANT: Healy, Aileen

; APPLICANT: Acton, Susan L.

; APPLICANT: Donoghue, Mary

; APPLICANT: Stagliano, Nancy

; APPLICANT: Perodin, Jacquelin

; APPLICANT: Rodrigue-Way, Amelie

; TITLE OF INVENTION: Methods and compositions for treating

; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,

; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,

; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,

; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,

; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,

; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2314,

; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,

; FILE REFERENCE: MPI02-018PIENOMNIN

; CURRENT APPLICATION NUMBER: US/10/353,690

; PRIOR FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: 60/353,224

; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/364,529

; PRIOR FILING DATE: 2002-03-15

; PRIOR APPLICATION NUMBER: 60/373,861

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; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 2393
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-99

Query Match          95.6%; Score 1670.4; DB 13; Length 2393;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCAGAGACATGAGAGGACAGCAGCGGAATGATCTCCAGCAAGAACACCTTCAGC 60
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QY 61 TGGAGCATCTCCAGCCAGGCACTCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGC 120
DB 138 TGGAGCATCTCCAGCCAGGCACTCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGC 197
QY 121 CCAGGCATCTCCAGCCAGGCACTCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGC 180
DB 198 CCAGGCATCTCCAGCCAGGCACTCTCCAGCTGGGACACCTCCAGGCGGGCATCTCCAGC 257
QY 181 CCAGGCATCTCCAGCTGGGTACACCTCCAGGCGGGCATCTCCAGGCGGGCATCTCCAGC 240
DB 258 CCAGGCATCTCCAGCTGGGTACACCTCCAGGCGGGCATCTCCAGGCGGGCATCTCCAGC 317
QY 241 CCAGGCATCTCCAGGCGGGCATCTCCAGCTGGGTACACCTCCAGGCGGGCATCTCCAGC 300
DB 318 CCAGGCATCTCCAGGCGGGCATCTCCAGCTGGGTACACCTCCAGGCGGGCATCTCCAGC 377
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DB 378 CAGGTCATCATCCGCGAGGTCCAGCTCCGCTGGGTACAACTCCGCAACAGAGGTACCTTGT 437
QY 361 TAGAGCAACACAGTGGGGGTGTACCCATCCGATCATCTCTGCGCAGGTCCAGCACAGC 420
DB 438 TAGAGCAACACAGTGGGGGTGTACCCATCCGATCATCTCTGCGCAGGTCCAGCACAGC 497
QY 421 AACAGGGCCACAGAGGAGCCAGGTACAGGCTCCGCAAGTTCACTTGGGCGGAGG 480
DB 498 AACAGGGCCACAGAGGAGCCAGGTACAGGCTCCGCAAGTTCACTTGGGCGGAGG 557
QY 481 CCAGAGCAGGTACCGCTCATCCGCTGGGTCCGCTCCCTCATTTGCCCTGGTGGTTCGCT 540
DB 558 CCAGAGCAGGTACCGCTCATCCGCTGGGTCCGCTCCCTCATTTGCCCTGGTGGTTCGCT 617
QY 541 CATCATCTCTTCCAGTCTTGGCAGGGCCACACAGGGATCAGGTACAGAGGAGGGA 600
DB 618 CATCATCTCTTCCAGTCTTGGCAGGGCCACACAGGGATCAGGTACAGAGGAGGGA 677
QY 601 GAGCTTCCCAAGCAGCTGTTCGTGTGACGGGGGTGGTGAAGCTGCAAGTGAAGTGA 660
DB 678 GAGCTTCCCAAGCAGCTGTTCGTGTGACGGGGGTGGTGAAGCTGCAAGTGAAGTGA 737
QY 661 CGAGCTGGGCTGGCTGAGGTTTGACTGGGACAGTCTCTGCTTAAATCTACTCTGGGTC 720
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DB 738 CGAGCTGGGCTGGCTGAGGTTTGACTGGGCAAGTCTCTGCTTAAATCTACTCTGGGTC 797
QY 721 CTCCTCATCAGTGGCTTCCCATCTGTAGCAGCACTTGAATGATCTCTACTCAGAGAGAC 780
DB 798 CTCCTCATCAGTGGCTTCCCATCTGTAGCAGCACTTGAATGATCTCTACTCAGAGAGAC 857
QY 781 CTGCCAGCAGCTGGGTTTCGAGAGTCTCAACGGAACACGAGGTTGCCACAGGATTT 840
DB 858 CTGCCAGCAGCTGGGTTTCGAGAGTCTCAACGGAACACGAGGTTGCCACAGGATTT 917
QY 841 TGCCCAACAGCTTCTCAATCTTCAGATACAACTCCACCATCCAGGAAGCTCCACAGGTC 900
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DB 978 TGAATGCCCTTCCCAAGCGGTATATCTCCCTCCAGTGTTCCTCACTGCGGACTGAGGGCCAT 1037
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DB 1038 GACCGGGCGGATCTGGTGGAGGGCGCTGGCTCGGATAGCAAGTGGCTTGGCAAGTGAG 1097
QY 1021 TCTGCACTTCGGGCAACCCACCATCTGTGGAGGCACTCTCATTTGAGCGCCAGTGGGTC 1080
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DB 1278 CAAACAGCAATTAACCGGATGAGGAGCACTATGATCATGCGCTCATGCGGCTTCCAA 1337
QY 1261 GCGCTTGAACCTTGTCCGCTCAATCCACCTGCTGCTCCCTCCCATGATGAGGAGACCTT 1320
DB 1338 GCGCTTGAACCTTGTCCGCTCAATCCACCTGCTGCTCCCTCCCATGATGAGGAGACCTT 1397
QY 1321 TAGCTTCAATGAGACCTGCTGGATCAAGGCTTGGCAAGACAGGAGACAGATGACAA 1380
DB 1398 TAGCTTCAATGAGACCTGCTGGATCAAGGCTTGGCAAGACAGGAGACAGATGACAA 1457
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DB 1458 GACATCCCTTCCCTCCGAGGAGTGCAGGTCAATCTCATGCACTTCAAGAAATGCAATGA 1517
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DB 1518 CTACTTGGTCTATGACAGTTTACCTTACCCCAAGGATGATGTGCTGGGAGCCTTGGTGG 1577
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DB 1578 GGGCAGAGACTCTCTGCGCAGGAGACAGCGGGGGGCTCTTGTCTGTGAGCAAGAACCG 1637
QY 1561 CTGTGTACCTGGCAGGTGTCAACGAGCTGGGGCAAGGCTGTGGCCAGAGAACTGG 1620
DB 1638 CTGTGTACCTGGCAGGTGTCAACGAGCTGGGGCAAGGCTGTGGCCAGAGAACTGG 1697
QY 1621 TGTGTACCAAAAGTGCAGAAAGTCTTCCCTGGATTTACGCAAGATGGAG 1672
DB 1698 TGTGTACCAAAAGTGCAGAAAGTCTTCCCTGGATTTACGCAAGATGGAG 1749
```

RESULT 3
US-09-888-615-45
; Sequence 45 Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:

APPLICANT: Quinn, Kerry E.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Majumder, Kumud
APPLICANT: Vernet, Corine
APPLICANT: Hermann, John L.
APPLICANT: Burgess, Catherine
APPLICANT: Fernandes, Elma
APPLICANT: Taupier Jr., Raymond
APPLICANT: Rastelli, Luca
APPLICANT: Curagen Corporation
APPLICANT: Gerlach, Valerie L.
APPLICANT: MacDougall, John R.
TITLE OF INVENTION: NOVEL SERINE/THRONINE PROTEIN-KINASE LIKE PROTEINS AND
FILE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: 15966-598 CIP
CURRENT APPLICATION NUMBER: US/09/898,837A
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 1314
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1263)
US-09-898-837A-14

Query Match 74.5%; Score 1302.8; DB 11; Length 1314;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1304; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	434	AGGAGAGCCAGGTACGAGCTGCCAAGTTCACTGGCGGAGGCGGAGAGAGAGCTA	493
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QY	494	CCGCTCATCGGGCGGTGCTCCCTCATTTGCTCCCTGCTGCTGCTCATCATCTCTTC	553
DB	61	CCGCTCATCGGGCGGTGCTCCCTCATTTGCTCCCTGCTGCTGCTCATCATCTCTTC	120
QY	554	CAGTTCTGGCAGGCGGCACACAGGGATCAGGTACAAGGAGCAGAGGAGAGCTGTCCCAAG	613
DB	121	CAGTTCTGGCAGGCGGCACACAGGGATCAGGTACAAGGAGCAGAGGAGAGCTGTCCCAAG	180
QY	614	CAGCTGTTGCTGTGACGCGGGGTGGTGAATGCAAGCTGAAGAGTGAAGAGCTGGGCTGC	673
DB	181	CAGCTGTTGCTGTGACGCGGGGTGGTGAATGCAAGCTGAAGAGTGAAGAGCTGGGCTGC	240
QY	674	GTGAGTTTACCTGGGAGCAAGTCTCTGCTTAAATCTACTGCTGCTCCCATCAGTGG	733
DB	241	GTGAGTTTACCTGGGAGCAAGTCTCTGCTTAAATCTACTGCTGCTCCCATCAGTGG	300
QY	734	CTTCCCATCTGTAGAGCAACTGGATGACTCTTACTCTCAGAGAAGACCTGCCAGCAGCTG	793
DB	301	CTTCCCATCTGTAGAGCAACTGGATGACTCTTACTCTCAGAGAAGACCTGCCAGCAGCTG	360

QY	794	GGTTTCGAGAGTGTCTCAACCGACAAACCGAGGTGGCCACAGGAGTTTTCACACAGCTTC	853
DB	361	GGTTTCGAGAGTGTCTCAACCGACAAACCGAGGTGGCCACAGGAGTTTTCACACAGCTTC	420
QY	854	TCATCTTTCAGATACAACTCCACCTCCAGGAAAGCTCCACAGTCTGAATGCCCTTCC	913
DB	421	TCATCTTTCAGATACAACTCCACCTCCAGGAAAGCTCCACAGTCTGAATGCCCTTCC	480
QY	914	CAGCGGTATATCTCCCTCCAGTGTTCCTGCGGACTGAGGCGCATGACCGGCGGATC	973
DB	481	CAGCGGTATATCTCCCTCCAGTGTTCCTGCGGACTGAGGCGCATGACCGGCGGATC	540
QY	974	GTGGAGGGCGCTGCGCTCCAGTATGCAAGTGGCTTTGGCAAGTGTGCTCTGCTCGGC	1033
DB	541	GTGGAGGGCGCTGCGCTCCAGTATGCAAGTGGCTTTGGCAAGTGTGCTCTGCTCGGC	600
QY	1034	ACCACCCACATCTGTGGAGGCGCTCATTTGAGCGCCAGTGGGTGCTCACTGCGGCCAC	1093
DB	601	ACCACCCACATCTGTGGAGGCGCTCATTTGAGCGCCAGTGGGTGCTCACTGCGGCCAC	660
QY	1094	TGCTTCTTCTGACCCCGGAGAGGTCTCTGGAGGGCTGGAAGGTGTACGCGGCGCACAGC	1153
DB	661	TGCTTCTTCTGACCCCGGAGAGGTCTCTGGAGGGCTGGAAGGTGTACGCGGCGCACAGC	720
QY	1154	AACCTGCAACGAGTTGCTGAGGAGCGCTCCATTTGCCAGATCATCATCAACAGCAATTAC	1213
DB	721	AACCTGCAACGAGTTGCTGAGGAGCGCTCCATTTGCCAGATCATCATCAACAGCAATTAC	780
QY	1214	ACCGATGAGGAGGAGGAGTATGACATCGCCCTCATCGGGCTGTCGAAGCCCTGAGCCCTG	1273
DB	781	ACCGATGAGGAGGAGGAGTATGACATCGCCCTCATCGGGCTGTCGAAGCCCTGAGCCCTG	840
QY	1274	TCGCTCACAATCCACCCCTGCTTGCCTCCCATGATGATGATGATGATGATGATGATGATG	1333
DB	841	TCGCTCACAATCCACCCCTGCTTGCCTCCCATGATGATGATGATGATGATGATGATGATG	900
QY	1334	ACCTGCTGATACACAGGCTTTGGCAAGACGAGGAGACAGATGACAGATGACAGATGACAG	1393
DB	901	ACCTGCTGATACACAGGCTTTGGCAAGACGAGGAGACAGATGACAGATGACAGATGACAG	960
QY	1394	CTCCGGAGGTGAGGTGATCTCATCTGAGTTCAGAAATGCAATGATGATGATGATGATGATG	1453
DB	961	CTCCGGAGGTGAGGTGATCTCATCTGAGTTCAGAAATGCAATGATGATGATGATGATGATG	1020
QY	1454	GACAGTTTACCTTACCCCAAGGATGATGTGTGCTGGGACCTCTGTTGGGGGAGAGACTCC	1513
DB	1021	GACAGTTTACCTTACCCCAAGGATGATGTGTGCTGGGACCTCTGTTGGGGGAGAGACTCC	1080
QY	1514	TGCCAGGAGACAGCGGGGGGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	1573
DB	1081	TGCCAGGAGACAGCGGGGGGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	1140
QY	1574	GGTGTCAACAGCTGGGGGACAGGCTGTGGCCAGAGAAACAAACCTGGTGTGTGTGTGTGTG	1633
DB	1141	GGTGTCAACAGCTGGGGGACAGGCTGTGGCCAGAGAAACAAACCTGGTGTGTGTGTGTGTG	1200
QY	1634	GTGACAGAGAGTTCTTCTCCCTGGATTTACAGCAAGTGGAGGCGGAGGTGCAATTCAGAAA	1693
DB	1201	GTGACAGAGAGTTCTTCTCCCTGGATTTACAGCAAGTGGAGGCGGAGGTGCAATTCAGAAA	1260
QY	1694	TCTTAACAGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	1739
DB	1261	TCTTAACAGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	1306

RESULT 5
US-09-898-837A-17/c
; Sequence 17, Application US/09898837A
; Publication No. US2003007697A1
; GENERAL INFORMATION:
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Spytek, Kimberly A.

; NUMBER OF SEQ ID NOS: 53			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 16			
; LENGTH: 1078			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-898-837A-16			
Query Match			
Best Local Similarity 61.1%; Score 1068.4; DB 11; Length 1078;			
Matches 1069; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	670	CTGCGTGAGGTTTGACTGGGCAAGAAGTCTCTGCTTAAATCTACTCTGGGTCTCCCATCA 729	
DB	1078	CTGCGTGAGGTTTGACTGGGCAAGAAGTCTCTGCTTAAATCTACTCTGGGTCTCCCATCA 1019	
QY	730	GTGGCTCCCATCTGTAGCAGCAACTGGGAATGACTCTCTACTCAGAGAAGACCTGCCAGCA 789	
DB	1018	GTGGCTCCCATCTGTAGCAGCAACTGGGAATGACTCTCTACTCAGAGAAGACCTGCCAGCA 959	
QY	790	GCTGGGTTTTCCAGAGTGCTCACCGGCAACCCGAGGTTGCCACAGGGAATTTTGCCAAACAG 849	
DB	958	GCTGGGTTTTCCAGAGTGCTCACCGGCAACCCGAGGTTGCCACAGGGAATTTTGCCAAACAG 899	
QY	850	CTTCTCAATCTTGAGATACAACTCCACCATCCAGGAAGCGCTCCACAGGTCCTGAATGCC 909	
DB	898	CTTCTCAATCTTGAGATACAACTCCACCATCCAGGAAGCGCTCCACAGGTCCTGAATGCC 839	
QY	910	TTCCACGCGTATATCTCCCTCCAGTGTTCCTCACTCGGACTGAGGCGCATGACCGGGCG 969	
DB	838	TTCCACGCGTATATCTCCCTCCAGTGTTCCTCACTCGGACTGAGGCGCATGACCGGGCG 779	
QY	970	GATCGTGGGAGGGCGCTGGCCCTCGGATAGCAAGTGCGCTTTGGCAAGTGAGTCTGCACTT 1029	
DB	778	GATCGTGGGAGGGCGCTGGCCCTCGGATAGCAAGTGCGCTTTGGCAAGTGAGTCTGCACTT 719	
QY	1030	CGGCACACCCACATCTGTGGAGGCAAGCTCATTTGAGCCCGACGTGGGTGCTCACTGCCG 1089	
DB	718	CGGCACACCCACATCTGTGGAGGCAAGCTCATTTGAGCCCGACGTGGGTGCTCACTGCCG 659	
QY	1090	CCACTGTCTTTCTGTGACCCGGGAGAAAGTCCCTGGAGGGCTGGAAGGTGTACCGGGCAC 1149	
DB	658	CCACTGTCTTTCTGTGACCCGGGAGAAAGTCCCTGGAGGGCTGGAAGGTGTACCGGGCAC 599	
QY	1150	CAGCAACTGCAACAGTTGCTGAGGAGCGCTCCATTGCCAGATCATCATCAACAGCAA 1209	
DB	598	CAGCAACTGCAACAGTTGCTGAGGAGCGCTCCATTGCCAGATCATCATCAACAGCAA 539	
QY	1210	TTACACCGATCAGAGAGACGACTATGACATCGCCCTCATGCGGCTGTCCAAAGCCCTGAC 1269	
DB	538	TTACACCGATCAGAGAGACGACTATGACATCGCCCTCATGCGGCTGTCCAAAGCCCTGAC 479	
QY	1270	CCTGTCCGCTCACATCCAACCTGTGTGCTTCCCTCCCATGCAATGGACAGACCTTTAGCCTCAA 1329	
DB	478	CCTGTCCGCTCACATCCAACCTGTGTGCTTCCCTCCCATGCAATGGACAGACCTTTAGCCTCAA 419	
QY	1330	TGAGACCTGTGGATCAAGGCTTTGGCAAGACCCAGGGAGACGATCAGCAAGCATCCCC 1389	
DB	418	TGAGACCTGTGGATCAAGGCTTTGGCAAGACCCAGGGAGACGATCAGCAAGCATCCCC 359	
QY	1390	CTTCTCCGGAGGTGCAAGTCAATCTCATCGACTTCAAGAAATGCAATGACTACTTGGT 1449	
DB	358	CTTCTCCGGAGGTGCAAGTCAATCTCATCGACTTCAAGAAATGCAATGACTACTTGGT 299	
QY	1450	CTATGACAGTTTACCTTACCCCAAGATGATGTGTGTGTGGAGACCTTCGTGGGGGACAGA 1509	
DB	298	CTATGACAGTTTACCTTACCCCAAGATGATGTGTGTGTGGAGACCTTCGTGGGGGACAGA 239	
QY	1510	CTTCTGCCAGGAGACACGCGGGGGCCCTTTGTCTGTGTGAGCAGAAACACCGCTGTACCT 1569	
DB	238	CTTCTGCCAGGAGACACGCGGGGGCCCTTTGTCTGTGTGAGCAGAAACACCGCTGTACCT 179	
QY	1570	GGCAGGTGTCAACAGCTGGGGCACAGGCTGTGGCCACAGAAACAAACCTGGTGTGTACAC 1629	

QY 891 TCACACAGGTCTGAATGCGCTTCCAGCGGTATATCTCCCTCCAGTGTTCACACTGCGGAC 950
Db 538 -----AGGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCACACTGCGGAC 592
QY 951 TGAGGGCCATGACCGGCGCATCTGTGGAGGGCGCTGGCTCGATAGCAAGTGGCCTT 1010
Db 593 TGAGGGCCATGACCGGCGCATCTGTGGAGGGCGCTGGCTCGATAGCAAGTGGCCTT 652
QY 1011 GGCAAGTGAATCTGCACTTCGGGACCAACCCACATCTGTGGAGGCAAGCTCATTTGACGCC 1070
Db 653 GGCAAGTGAATCTGCACTTCGGGACCAACCCACATCTGTGGAGGCAAGCTCATTTGACGCC 712
QY 1071 AGTGGGTGCTCACTGCGGCCCATCTGCTTCTGTGACCCCGGAGAAAGTCTGGAGGCT 1130
Db 713 AGTGGGTGCTCACTGCGGCCCATCTGCTTCTGTGACCCCGGAGAAAGTCTGGAGGCT 772
QY 1131 GGAAGGTGTACGGGGCACAGCAACTGACCAAGTTGCTGAGGAGCAAGCTCCATTGCCG 1190
Db 773 GGAAGGTGTACGGGGCACAGCAACTGACCAAGTTGCTGAGGAGCAAGCTCCATTGCCG 832
QY 1191 AGATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATGCGCCCTCATGC 1250
Db 833 AGATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATGCGCCCTCATGC 892
QY 1251 GGCTGTCCAAGCCCTGACCCCTGCTGCTGCTCATCTCCACCTGCTGCTGCTGCTGCTGCTG 1310
Db 893 GGCTGTCCAAGCCCTGACCCCTGCTGCTGCTCATCTCCACCTGCTGCTGCTGCTGCTGCTG 952
QY 1311 GACAGACCTTTAGCTCAATGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1370
Db 953 GACAGACCTTTAGCTCAATGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1012
QY 1371 CAGATGACAGACATCCCTTCTGCGGAGGTGCGAGGTCAATCTCATGACATTCAGAA 1430
Db 1013 CAGATGACAGACATCCCTTCTGCGGAGGTGCGAGGTCAATCTCATGACATTCAGAA 1072
QY 1431 AATCGATGACTACTGTGCTATGACAGTTACTTACCCAGGATGATGCTGCTGCTGCTGCTG 1490
Db 1073 AATCGATGACTACTGTGCTATGACAGTTACTTACCCAGGATGATGCTGCTGCTGCTGCTG 1132
QY 1491 ACCTTCTGCGGGCAGAGACTCTGCGCAGGAGGACAGCGGGGGCTCTTCTGCTGCTGCTG 1550
Db 1133 ACCTTCTGCGGGCAGAGACTCTGCGCAGGAGGACAGCGGGGGCTCTTCTGCTGCTGCTG 1192
QY 1551 AGAACACCGCTGTGTAATCTGACAGGTGTCACAGCTGGGGCAGAGCTGTGGCCAGAGAA 1610
Db 1193 AGAACACCGCTGTGTAATCTGACAGGTGTCACAGCTGGGGCAGAGCTGTGGCCAGAGAA 1252
QY 1611 ACAACCTGTGTGTACACCAAGTGCAGAAAGTTCTTCCCTGATTTTACAGCAAGATGG 1670
Db 1253 ACAACCTGTGTGTACACCAAGTGCAGAAAGTTCTTCCCTGATTTTACAGCAAGATGG 1312
QY 1671 AGAGCGAGGTGCGATTCAGAAATCCCTAA 1699
Db 1313 AGAGCGAGGTGCGATTCAGAAATCCCTAA 1341

RESULT 9

US-09-879-792-35

; Sequence 35, Application US/09879792

; Patent No. US20020061850A1

; GENERAL INFORMATION:

; APPLICANT: Xiao, Yonhong

; APPLICANT: Gedrich, Richard

; TITLE OF INVENTION: Regulation of Human Transmembrane Serine

; TITLE OF INVENTION: Protease

; FILE REFERENCE: 02973.00035

; CURRENT APPLICATION NUMBER: US/09/879,792

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/211,224

; PRIOR FILING DATE: 2000-06-13

; PRIOR APPLICATION NUMBER: US 60/283,353

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/283,648
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT _____ (Docket No. US20020061850A1 LIO-81-WO)
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 35

; LENGTH: 1230

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(1230)

; OTHER INFORMATION: n = A, T, C or G

; US-09-879-792-35

Query Match 60.2%; Score 1053; DB 9; Length 1230;

Best Local Similarity 92.1%; Pred. No. 1.3e-291;

Matches 1134; Conservative 0; Mismatches 84; Indels 13; Gaps 2;

QY 521 ATTGCCCTGTGTGTTTCGCTCATCATCTCTTCAGTTCTGGGAGGGCCACACAGGGATC 580

Db 1 ATGACCCAGCTGTCTGCTTCTTTTCTCTAGTCCAGTTCTGGCAGNNCCACACAGNNATC 60

QY 581 AGGTACAGGAGCAGAGGAGGAGCTGTCCAGCAGCTGTCCGTGTGACGGGGTGTG 640

Db 61 AGGTACAGGAGCAGAGGAGGAGCTGTCCAGCAGCTGTCCGTGTGACGGGGTGTG 120

QY 641 GACTGCAAGCTGAAAGAGTGCAGAGCTGGGCTGCGTGCAGGTTTGACTGGGACAACTCTCTG 700

Db 121 GACTGCAAGCTGAAAGAGTGCAGAGCTGGGCTGCGTGCAGGTTTGACTGGGACAACTCTCTG 180

QY 701 CTTAAAAATCTACTCTGGGTCTCTCCATCAGTGTGCTTCCATCTGTAGCAGCAACTGTGAAT 760

Db 181 CTTAAAAATCTACTCTGGGTCTCTCCATCAGTGTGCTTCCATCTGTAGCAGCAACTGTGAAT 240

QY 761 GACTCCTACTCTGAGAGAGAGCTGTCCAGCAGCTGTGGTTTCGAGAGTGTCTCCGAGCAACC 820

Db 241 GACTCCTACTCTGAGAGAGAGCTGTCCAGCAGCTGTGGTTTCGAGAGTGTCTCCGAGCAACC 300

QY 821 GAGGTGCCCCACAGGGATTTTGCCAAAGCTTCTCAATCTTGAGATACAACTCCACCAATC 880

Db 301 GAGGTGCCCCACAGGGATTTTGCCAAAGCTTCTCAATCTTGAGATACAACTCCACCAATC 360

QY 881 CAGAAAAAGCTTCCACAGGTCTGAAATGCTTCCAGCGGTATATCTCCCTCCAGTGTTC 940

Db 361 CAGAAAAAGCTTCCACAGGTCTGAAATGCTTCCAGCGGTATATCTCCCTCCAGTGTTC 420

QY 941 CACTGCGGACTGTAGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCGGATAGC 1000

Db 421 CACTGCGGACTGTAGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCGGATAGC 480

QY 1001 AAGTGGCTTTGGCAAGTGAAGTCTGCACCTTGGGCAACCAACCCACATCTGTGGAGGCAAGCTC 1060

Db 481 AAGTGGCTTTGGCAAGTGAAGTCTGCACCTTGGGCAACCAACCCACATCTGTGGAGGCAAGCTC 540

QY 1061 ATTGACGCCCAAGTGGGTGCTCACTGCGGCCCACTGTCTTCTTCTGTAACCCGGAGAGGTTC 1120

Db 541 ATTGACGCCCAAGTGGGTGCTCACTGCGGCCCACTGTCTTCTTCTGTAACCCGGAGAGGTTC 600

QY 1121 CTGGAGGGCTGGAAGGTGTAGCGGGCCACCGAGCAACCTGCAACCTGCTGTGGGCGAGCTC 1180

Db 601 CTGGAGGGCTGGAAGGTGTAGCGGGCCACCGAGCAACCTGCAACCTGCTGTGGGCGAGCTC 660

QY 1181 TCCATTGCCAGATCATCATCAACAGCAATTTACACCATGAGGAGGAGCACTATGACATC 1240

Db 661 TCCATTGCCAGATCATCATCAACAGCAATTTACACCATGAGGAGGAGCACTATGACATC 720

QY 1241 GCCCTCATGCGGCTGTCCAAAGCCCTTGAACCTGTGCGGTCACTCCACCCCTGCTGCTC 1300

Db 721 GCCCTCATGCGGCTGTCCAAAGCCCTTGAACCTGTGCGGTCACTCCACCCCTGCTGCTC 780

QY 1301 CCCATGATGACAGACCTTTAGCTCTCAATGAGAGACCTGTGGATCAGAGGCTTTGGCA- 1359

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Db      781  TCCTCTGCCCCAGCCCCAGACCCCTCTGCGACCCCTCGACTTGTGAGCATCTGTCAAC 840
QY      1360  -----GACCAGGGAGACAGATGACAGACATCCCTCTCCCTCCGGAGGTCCAG 1408
Db      841  TCATATCCGGGCCCCAAGCTTCTGCAGACAGACATCCCTCTCCCTCCGGAGGTCCAG 900
QY      1409  GTCAATCTCATCGACTTCAAGAAATGCAATGACTTGTGCTATGACAGTTACTTACC 1468
Db      901  GTCAATCTCATCGACTTCAAGAAATGCAATGACTTGTGCTATGACAGTTACTTACC 960
QY      1469  CCAAGAGTATGATGTGTGCTGGGACCTTCTGTGGGGGACAGACTCTCTCCAGGGAGACAGC 1528
Db      961  CCAAGAGTATGATGTGTGCTGGGACCTTCTGTGGGGGACAGACTCTCTCCAGGGAGACAGC 1020
QY      1529  GGGGGGCTCTTGTGTGTGAGCAGAACCAACCGCTGTACTCTGCGAGGTGTCACAGCTGG 1588
Db      1021  GGGGGGCTCTTGTGTGTGAGCAGAACCAACCGCTGTACTCTGCGAGGTGTCACAGCTGG 1080
QY      1589  GGACAGGCTGTGCGCCAGAGAAACAAACCTGTGTGTACACCAAAAGTGACAGAAAGTTCTT 1648
Db      1081  GGACAGGCTGTGCGCCAGAGAAACAAACCTGTGTGTGTACACCAAAAGTGACAGAAAGTTCTT 1140
QY      1649  CCCTGGATTTACAGCAAGATGAGAGCGAGGTGCGATTCAGAAAATCTTAACCGAGCTGGC 1708
Db      1141  CCCTGGATTTACAGCAAGATGAGAGCGAGGTGCGATTCAGAAAATCTTAACCGAGCTGGC 1199
QY      1709  CTGCTGTCTCTGACAGCACCGCTGCTGTGA 1739
Db      1200  CTGCTGTCTCTGACAGCACCGCTGCTGTGA 1230

RESULT 10
US-09-804-156-5
; Sequence 5, Application US/09804156
; Patent No. US20020068320A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT005P4
; CURRENT APPLICATION NUMBER: US/09/804,156
; PRIORITY FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/189,025
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-804-156-5

Query Match      44.8%; Score 782.4; DB 9; Length 1222;
Best Local Similarity 99.9%; Pred. No. 5,5e-214;
Matches 783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      892  CCACAGGCTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGCGACT 951
Db      9      CCACAGGCTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGCGACT 68
QY      952  GAGGGCCATGACCGGGCGGATCTGGAGGGGCGCTGGCTCGGATAGCAAGTGGCCTTG 1011
Db      69  GAGGGCCATGACCGGGCGGATCTGGAGGGGCGCTGGCTCGGATAGCAAGTGGCCTTG 128
QY      1012  GCAAGTGTGCTGTGCTCGGACCAACCACTGTGTGAGGACCGCTCATTTGACGCCCA 1071
Db      129  GCAAGTGTGCTGTGCTCGGACCAACCACTGTGTGAGGACCGCTCATTTGACGCCCA 188
QY      1072  GTGGGTGTCTCACTGCGGCCACTGTCTTCTGTGACCCCGGAGAGAGGTCTCTGAGGGCTG 1131
Db      189  GTGGGTGTCTCACTGCGGCCACTGTCTTCTGTGACCCCGGAGAGAGGTCTCTGAGGGCTG 248
QY      1132  GAAGGTGTAGGGGGGACCAAGCACTGTGACCAAGTGTGCTGAGGACCGCTCCATTGCCGA 1191

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Db      249  GAAGGTGTATCGCGGGACCCAGCAACCTGCAACCTGCTTGCCTGAGGACGCTCCATTGCCGA 308
QY      1192  GATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATCGCCCTTCATGCG 1251
Db      309  GATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATCGCCCTTCATGCG 368
QY      1252  GCTGTCCAAAGCCCTGACCCCTGCTGCGCTCAATCCACCCCTGCTTGCCTCCCATGCGATGG 1311
Db      369  GCTGTCCAAAGCCCTGACCCCTGCTGCGCTCAATCCACCCCTGCTTGCCTCCCATGCGATGG 428
QY      1312  ACAGACCTTTAGCTCAATGAGACCTGCTGATGACAGGCTTTTGGCAAGACCCAGGAGAC 1371
Db      429  ACAGACCTTTAGCTCAATGAGACCTGCTGATGACAGGCTTTTGGCAAGACCCAGGAGAC 488
QY      1372  AGATGACAGACATCCCTCTTCCCGGAGGTGCGAGTCAATCTCATCGACTTCAAGAA 1431
Db      489  AGATGACAGACATCCCTCTTCCCGGAGGTGCGAGTCAATCTCATCGACTTCAAGAA 548
QY      1432  ATGCAATGACTTACTTGTGTATGACAGTTACTTACCCCAAGGATGATGTGTGCTGGGGA 1491
Db      549  ATGCAATGACTTACTTGTGTATGACAGTTACTTACCCCAAGGATGATGTGTGCTGGGGA 608
QY      1492  CCTTCGTGGGGGACAGACTCTCTGCGAGGAGACAGCGGGGGGCTCTTGTGTGAGCA 1551
Db      609  CCTTCGTGGGGGACAGACTCTCTGCGAGGAGACAGCGGGGGGCTCTTGTGTGAGCA 668
QY      1552  GAACAACCGCTGTGTACTCTGCGAGGAGTGTACAGGCTGGGGGACAGGCTGTGTGCGGAGAAA 1611
Db      669  GAACAACCGCTGTGTACTCTGCGAGGAGTGTACAGGCTGGGGGACAGGCTGTGTGCGGAGAAA 728
QY      1612  CAAACCTGGTGTGTACACCAAAAGTGACAGAAAGTCTTCCCTGGATTTACAGCAAGATGGA 1671
Db      729  CAAACCTGGTGTGTACACCAAAAGTGACAGAAAGTCTTCCCTGGATTTACAGCAAGATGGA 788
QY      1672  GAGC 1675
Db      789  GAAC 792

RESULT 11
US-09-946-633-3
; Sequence 3, Application US/09946633
; Patent No. US20020119925A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: PT005P1
; FILE REFERENCE: Serine proteases
; CURRENT APPLICATION NUMBER: US/09/946,633
; PRIORITY FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 60/133,239
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/135,163
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/147,005
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/152,935
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/162,979
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-633-3

Query Match      44.8%; Score 782.4; DB 10; Length 1222;
Best Local Similarity 99.9%; Pred. No. 5,5e-214;
Matches 783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

892 CCACAGGCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACT 951
Db 9 CCACAGGCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACT 68
952 GAGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCGGATAGCAAGTGGCTTG 1011
Db 69 GAGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCGGATAGCAAGTGGCTTG 128
1012 GCAAGTGAAGTCTGCACTTCCGACACCAACCAATCTGTGGAGGCAAGTCTCATTCAGCCCA 1071
Db 129 GCAAGTGAAGTCTGCACTTCCGACACCAACCAATCTGTGGAGGCAAGTCTCATTCAGCCCA 198
1072 GTGGGTGCTCATCTGCGGCCCATCTGCTTCTGTGACCCCGGAGAAAGTCTCTGAGGGCTG 1131
Db 189 GTGGGTGCTCATCTGCGGCCCATCTGCTTCTGTGACCCCGGAGAAAGTCTCTGAGGGCTG 248
1132 GAAAGTGAAGTCTGCACTTCCGACACCAACCAATCTGTGGAGGCAAGTCTCATTCAGCCCA 1191
Db 249 GAAAGTGAAGTCTGCACTTCCGACACCAACCAATCTGTGGAGGCAAGTCTCATTCAGCCCA 308
1192 GATCATCATCAACAGCAATATACACCGATGAGGAGGAGCAATATGACATCGCCCTCATGCG 1251
Db 309 GATCATCATCAACAGCAATATACACCGATGAGGAGGAGCAATATGACATCGCCCTCATGCG 368
1252 GCTGTCCAAAGCCCTGACCTGTCGGCTCATCTCCAGTCTGCTGCTCCCAATGANGG 1311
Db 369 GCTGTCCAAAGCCCTGACCTGTCGGCTCATCTCCAGTCTGCTGCTCCCAATGANGG 428
1312 ACAGAGCTTTAGCTTCAATGAGACCTGCTGCGATCACAGGCTTTGGCAAGACCAAGGAGAC 1371
Db 429 ACAGAGCTTTAGCTTCAATGAGACCTGCTGCGATCACAGGCTTTGGCAAGACCAAGGAGAC 488
1372 AGATGACAGACATCCCTTCTCCGCGAGGTGCAAGTCAATCTCATGACATTCAGAA 1431
Db 489 AGATGACAGACATCCCTTCTCCGCGAGGTGCAAGTCAATCTCATGACATTCAGAA 548
1432 ATGCAATGACTACTTGTGTATGACAGTTACCTTACCCCAAGAGATGATGTGCTGGGA 1491
Db 549 ATGCAATGACTACTTGTGTATGACAGTTACCTTACCCCAAGAGATGATGTGCTGGGA 608
1492 CCTTCTGCGGGGAGAGACTCTGCGACGAGGAGACAGCGGGGGCTCTTCTGTGAGCA 1551
Db 609 CCTTCTGCGGGGAGAGACTCTGCGACGAGGAGACAGCGGGGGCTCTTCTGTGAGCA 668
1552 GAAACACCGCTGTGATCCTGGCAGGTGTACAGGCTGGGGGCAAGGCTGTGGCCAGAGAA 1611
1612 CAAACCTGGTGTATACCAAGAGTACAGAGTTCTTCCCTGGAATTTACAGCAAGATGGA 1671
Db 729 CAAACCTGGTGTATACCAAGAGTACAGAGTTCTTCCCTGGAATTTACAGCAAGATGGA 788
1672 GAGC 1675
Db 789 GAAC 792

RESULT 12
US-10-319-519-5
; Sequence 5, Application US/10319519
; Publication No. US20030175938A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; FILE REFERENCE: PT005P5
; CURRENT APPLICATION NUMBER: US/10/319,519
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 10/125,459
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 09/597,842
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 09/597,843

PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 10/067,761
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 09/946,633
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US 09/804,156
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: US 09/597,839
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/US00/12207
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/189,025
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: US 60/162,979
PRIOR FILING DATE: 1999-11-01
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 1222
TYPE: DNA
ORGANISM: Homo sapiens
US-10-319-519-5

Query Match 44.8%; Score 782.4; DB 13; Length 1222;
Best Local Similarity 99.9%; Pred. No. 5.5e-214;
Matches 783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 892 CCACAGGCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACT 951
Db 9 CCACAGGCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACT 68
QY 952 GAGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCGGATAGCAAGTGGCTTG 1011
Db 69 GAGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCGGATAGCAAGTGGCTTG 128
QY 1012 GCAAGTGAAGTCTGCACTTCCGACACCAACCAATCTGTGGAGGCAAGTCTCATTCAGCCCA 1071
Db 129 GCAAGTGAAGTCTGCACTTCCGACACCAACCAATCTGTGGAGGCAAGTCTCATTCAGCCCA 188
QY 1072 GTGGGTGCTCATCTGCGGCCCATCTGCTTCTGTGACCCCGGAGAAAGTCTCTGAGGGCTG 1131
Db 189 GTGGGTGCTCATCTGCGGCCCATCTGCTTCTGTGACCCCGGAGAAAGTCTCTGAGGGCTG 248
QY 1132 GAAAGTGAAGTCTGCACTTCCGACACCAACCAATCTGTGGAGGCAAGTCTCATTCAGCCCA 1191
Db 249 GAAAGTGAAGTCTGCACTTCCGACACCAACCAATCTGTGGAGGCAAGTCTCATTCAGCCCA 308
QY 1192 GATCATCATCAACAGCAATATACACCGATGAGGAGGAGCAATATGACATCGCCCTCATGCG 1251
Db 309 GATCATCATCAACAGCAATATACACCGATGAGGAGGAGCAATATGACATCGCCCTCATGCG 368
QY 1252 GCTGTCCAAAGCCCTGACCTGTCGGCTCATCTCCAGTCTGCTGCTCCCAATGANGG 1311
Db 369 GCTGTCCAAAGCCCTGACCTGTCGGCTCATCTCCAGTCTGCTGCTCCCAATGANGG 428
QY 1312 ACAGAGCTTTAGCTTCAATGAGACCTGCTGCGATCACAGGCTTTGGCAAGACCAAGGAGAC 1371
Db 429 ACAGAGCTTTAGCTTCAATGAGACCTGCTGCGATCACAGGCTTTGGCAAGACCAAGGAGAC 488
QY 1372 AGATGACAGACATCCCTTCTCCGCGAGGTGCAAGTCAATCTCATGACATTCAGAA 1431
Db 489 AGATGACAGACATCCCTTCTCCGCGAGGTGCAAGTCAATCTCATGACATTCAGAA 548
QY 1432 ATGCAATGACTACTTGTGTATGACAGTTACCTTACCCCAAGAGATGATGTGCTGGGA 1491
Db 549 ATGCAATGACTACTTGTGTATGACAGTTACCTTACCCCAAGAGATGATGTGCTGGGA 608
QY 1492 CCTTCTGCGGGGAGAGACTCTGCGACGAGGAGACAGCGGGGGCTCTTCTGTGAGCA 1551
Db 609 CCTTCTGCGGGGAGAGACTCTGCGACGAGGAGACAGCGGGGGCTCTTCTGTGAGCA 668
QY 1552 GAAACACCGCTGTGATCCTGGCAGGTGTACAGGCTGGGGGCAAGGCTGTGGCCAGAGAA 1611

Db 249 GAAGGTGTACGGGGACCAAGCACTGCTGCAAGTGTGCTGAGGAGCGCTCCATGCGGA 308
Qy 1192 GATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATCGCCCTCATGCG 1251
Db 309 GATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATCGCCCTCATGCG 368
Qy 1252 GCTGTCCAAAGCCCTGACCCCTGTCATCCATCAATCAACCCCTGCTTCCCTCCCATGCAATGG 1311
Db 369 GCTGTCCAAAGCCCTGACCCCTGTCATCCATCAATCAACCCCTGCTTCCCTCCCATGCAATGG 428
Qy 1312 ACAGACCTTTAGCTCAATGAGACCTGCTGGATCAACAGGCTTTGGCAAGACCGAGGAGAC 1371
Db 429 ACAGACCTTTAGCTCAATGAGACCTGCTGGATCAACAGGCTTTGGCAAGACCGAGGAGAC 488
Qy 1372 AGATGACAAAGACATCCCTTCCCTCCGGAGGTCAGGTCAATCTCATCGACTTCAAGAA 1431
Db 489 AGATGACAAAGACATCCCTTCCCTCCGGAGGTCAGGTCAATCTCATCGACTTCAAGAA 548
Qy 1432 ATGCAATGACTACTTGTGTATGACAGTTACTTACCCCAAGGATGATGTGTCTGGGGA 1491
Db 549 ATGCAATGACTACTTGTGTATGACAGTTACTTACCCCAAGGATGATGTGTCTGGGGA 608
Qy 1492 CCTTCGTGGGGGACAGACTCCTGCCAGGGAGACAGCGGGGGGCTCTTGTCTGTGAGCA 1551
Db 609 CCTTCGTGGGGGACAGACTCCTGCCAGGGAGACAGCGGGGGGCTCTTGTCTGTGAGCA 668
Qy 1552 GAACAACCGCTGTGTPACCTGTGGCAGGTGTCCAGCTGGGGGACAGCGCTGTGGCCAGAGAAA 1611
Db 669 GAACAACCGCTGTGTPACCTGTGGCAGGTGTCCAGCTGGGGGACAGCGCTGTGGCCAGAGAAA 728
Qy 1612 CAACCTGTGTGTATACCAACCAAGTGACAGAAAGTTCTTCCCTGGATTTACAGCAAGATGGA 1671
Db 729 CAACCTGTGTGTATACCAACCAAGTGACAGAAAGTTCTTCCCTGGATTTACAGCAAGATGGA 788
Qy 1672 GAGC 1675
Db 789 GAAC 792

RESULT 15
US-09-879-792-28
; Sequence 28, Application US/09879792
; Patent No. US20020061850A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Transmembrane Serine
; FILE OF INVENTION: Profease
; FILE REFERENCE: 02973.00035
; CURRENT APPLICATION NUMBER: US/09/879,792
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/211,224
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/283,353
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,648
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-879-792-28

Query Match 40.6%; Score 709.4; DB 9; Length 834;
Best Local Similarity 95.4%; Pred. No. 4.2e-193;
Matches 795; Conservative 0; Mismatches 31; Indels 7; Gaps 6;
Qy 664 GCTGGGCTGCTGAGGTTTGACTGGGACAAAGTCTCTGCTTAAATCTACTCTGGGTCTC 723

Db 1 GCTGGGCTGCTGAGGTTTGACTGGGACAAAGTCTCTGCTTAAATCTACTCTGGGTCTC 60
Qy 724 CCATCAGTGGCTTCCCATCTGTAGCAGCAACTGGAATGACTCTCTACTCAGAGAGACCTG 783
Db 61 CCATCAGTGGCTTCCCATCTGTAGCAGCAACTGGAATGACTCTCTACTCAGAGAGACCTG 120
Qy 784 CCAGCAGCTGGTTCAGAGAGTCTCAACCGGACAAACCGAGGTTGCCACAGGATTTTGC 843
Db 121 CCAGCAGCTGGTTCAGAGAGTCTCAACCGGACAAACCGAGGTTGCCACAGGATTTTGC 180
Qy 844 CAACAGCTTCTCAATCTTGAATACAACTCCACCATCCAGGAAAGCCTCCACAGGTCTGA 903
Db 181 CAACAGCTTCTCAATCTTGAATACAACTCCACCATCCAGGAAAGCCTCCACAGGTCTGA 240
Qy 904 ATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCACCTGCGGACTGAGGGCCATGAC 963
Db 241 ATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCACCTGCGGACTGAGGGCCATGAC 300
Qy 964 CGGCGGATCTGTGGAGGGGCGCTGGCTCGGATAGCAAGTGGCTTGGCAAGTGAATCT 1023
Db 301 CGGCGGATCTGTGGAGGGGCGCTGGCTCGGATAGCAAGTGGCTTGGCAAGTGAATCT 360
Qy 1024 GCATTCGGGACACACCCACATCTGTGGAGGCAAGCTCATTTGACGCCAGTGGGTCTCAC 1083
Db 361 GCATTCGGGACACACCCACATCTGTGGAGGCAAGCTCATTTGACGCCAGTGGGTCTCAC 420
Qy 1084 TGCCCGCCACTGCTTCTTGTGACCCGGGAGAGGTCCTGAGGGGCTGGAAGGTGTACGC 1143
Db 421 TGCCCGCCACTGCTTCTTGTGACCCGGGAGAGGTCCTGAGGGGCTGGAAGGTGTACGC 480
Qy 1144 GGGCACAGCAACTGCAACAGTTGCTGAGGAGGCTTCCATTCGAGATCATCATCAA 1203
Db 481 GGGCACAGCAACTGCAACAGTTGCTGAGGAGGCTTCCATTCGAGATCATCATCAA 538
Qy 1204 CAGCAATTTACCCGATGAGGAGGAGGACTA-TGACATGGCCCTCATGCGGCTGTCCAAGC 1262
Db 539 CAGCAATTTACCCGATGAGGAGGAGGACTA-TGACATGGCCCTCATGCGGCTGTCCAAGC 598
Qy 1263 CCCTGACCTGTGCTGCTCATCCACCTGCTTGCCT-CCCATGCTGAGGACAGACCTTT 1321
Db 599 CCCTGAGACCTGTGCTGCTCATCCACCTGCTTGCCTCCCATGCTGAGGAGGAGGAGG 658
Qy 1322 AGCTCAATGAGACCTGCTGATCAAGGCTTTGGCAAGACAGGAGGAGAGATGACAAG 1381
Db 659 AGCTCAATGAGACCTGCTGATCAAGGCTTTGGCAAGACAGGAGGAGAGATGACAAG 718
Qy 1382 ACATCCCTTCTCCCGGAGGTCAGGTCAATCTCATCGACTTCAGAAATGCATGAC 1441
Db 719 ACATCCCTTCTCCCGGAGGTCAGGTCAATCTCATCGACTTCAGAAATGCATGAC 777
Qy 1442 TACTTGTCTATGACAGTTTACCCCAAGGATGATGTGTCTGGGGACT 1494
Db 778 TACTTGTCTATGACAGT--ACCTTACCCAGGATGATGTGTGTGGGAACTT 828

Search completed: December 17, 2003, 20:19:34
Job time : 535 secs

301 CAAACAGATTACACCGATGAGGAGGACGACTATGACATCGCCCTCATGCGGCTGTTCAA 360
1261 GCCCTGACCC 1271
361 GCCCCTTGACC 371

RESULT 2
US-09-008-271A-18
; Sequence 18, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF INVENTIONS: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2038 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNNOT13
; CLONE: 1337018
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-008-271A-18

Query Match 11.1%; Score 193.2; DB 3; Length 2038;
Best Local Similarity 55.8%; Pred. No. 8.3e-39;
Matches 435; Conservative 0; Mismatches 333; Indels 12; Gaps 3;

924 TCTCCCTCCAGTTTCCCATCGAGCTGAGGCGCCATGACCGGCGGATCGTGGAGGCG 983
759 TCTCCCTGCACCTGTCTTGCCTGTGGGAGAGCTGAGACCCCTGTTGGTGGTGGG 818
984 CGCTGGCTCGATAGCAGTGGCTTGCAGTGAAGTGCAGTTCGGCACCACCCACA 1043
819 AGGAGGCTCTGTGGAATTTGGCTTGGCCCTGAGGATCAGCATCCAGCAAAACGACG 878
1044 TCTGTGGAGGACCGCTCATTTGACGCGCCAGTGGGTGCTCACTCCGCCCACTCTCTTCG 1103
879 TCTGTGGAGGAGCATCTTGGACCCCACTGGGCTCTCAAGCAGCCCACTGCTTC 934

1104 TGAACCCGGGAGAGGTCCTGGAAGGCTGGAAGGTGTACGCGGGCCACGACAACTGCACC 1163
935 --AGGAAACATACCGATGTCTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGCA 992
1164 AGTTGCTGAGGAGCGCTCCATTGCGGAGATCATCATCAACAGCAATTATACCGATGAGG 1223
993 GCTTCCC---ATCCCTGGCTGTGGCCAAAGATCATCATTTGAATTCAACCCCATGACC 1049
1224 AGGACGACTATGACATCGCCCTCATGCGGCTGTCCAAGCCCTGACACCTGTGCCCTCACA 1283
1050 CCAAGACATGACATCGCCCTCATGAGCTGTGAGTTCCCACTCACTTTCTCAGGCACAG 1109
1284 TCACCCCTGCTTGCCTCCCATGATGAGACAGACCTTTAGCCTCAATGAGACCTGCTGGA 1343
1110 TCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGA 1169
1344 TCAGGCTTTGGCAGACAGGAGGACAGATGACAGACATCCCTTCTCTCCGGGAGG 1403
1170 TCATTGGATGGGCTTTTACGAAGCAGAAATGGAGGGAAGATGTTGACATATCTGTCAGG 1229
1404 TGCAGGTCAATCTCATCGACTTCAAGAAATGCAATGACTACTTGGTCTATGACAGTTACC 1463
1230 CGTCAGTCCAGGTCAATGACAGACACGCTGCAATGACAGAGTGCCTACAGGGGAG 1289
1464 TTACCCCAAGGATGATGTGCTGGGACCTTCTGTTGGGCGAGAGACTTCTTCCAGGGAG 1523
1290 TCACCGAGAAAGATGTGTGACAGCATCCCGAAGGGGTGTGGAACACCTGCCAGGGTG 1349
1524 ACAGGGGGGCTCTTGTCTGTGAGCAGAAACACCTGCTGCTACCTGCGAGGTGTACCA 1583
1350 ACAGTGGTGGGCTCCCTGATGT---ACCAATCTGACCCAGTGTGTTGTTGTTGTTA 1406
1584 GCTGGGCGACAGGCTGTGGGCGCAGAGAAACAACTGCTGTGTATACCAAAAGTGACAGA 1643
1407 GCTGGGCTATGCTGTGGGGGCGGAGCAGCCAGGATATACCAAGGTCTCAGCCT 1466
1644 TTCTTCCCTGGATTTACAGCAAGATGAGAGCGAGGTGCGGATTCAGAAAATCTTAACAG 1703
1467 ATCTCAACTGGATCTCAAAATGCTGGAAGGCTGAGCTGTATGCTGCTGCCCTTTGCAG 1526

RESULT 3
US-09-656-002-1
; Sequence 1, Application US/09656002
; Patent No. 6455668
; GENERAL INFORMATION:
; APPLICANT: Mack, David
; APPLICANT: Gish, Kurt
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AN
; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
; FILE REFERENCE: A-69108/DJB/JJD/AMS
; CURRENT APPLICATION NUMBER: US/09/656,002
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 09/525,993
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 09/493,444
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US 00/07044
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-656-002-1

Query Match 11.1%; Score 193.2; DB 4; Length 2079;
Best Local Similarity 55.8%; Pred. No. 8.3e-39;
Matches 435; Conservative 0; Mismatches 333; Indels 12; Gaps 3;

924	Qy	TTCTCCCTCCAGTGTTCCTCACTGCGGACTGAGGGCCATGACACGGGGCGGATCTGTGGGAGGGG	983
925	Qy	TTCTCCCTCCAGTGTTCCTCACTGCGGACTGAGGGCCATGACACGGGGCGGATCTGTGGGAGGGG	984
774	Db	TTCTCCCTGCACCTGTCTTGGCTGTGGGAAGAGCCCTGAGACCCCCCGTGTGTGGTGGGTGGGG	833
984	Qy	CGCTGGCCCTCGGATAGCAAGTGGCCTTTGGCAAGTGTAGTCTGTGACTTTCGGGCACACCCACCA	1043
834	Db	AGAGGGCCTCTGTGGATTCTTGGCCTTTGGCAAGTGTAGTCTGTGACTTTCGGGCACCAACAGCAGC	893
1044	Qy	TTCTGTGGAGCAGCGCTCATTGACGCCCACTGGGTGTCTCACTGCGGCCCACTGTTCTTTCTG	1103
894	Db	TTCTGTGGAGGAGCATCTCTGACCCCACTGGGTCTCTCACGGCAGGCCCACTGCTTCTC---	949
1104	Qy	TGACCCGGGAGAGGTCTCTGGAGGGCTGGAGGTGTACGGGGGCAACAGGAACTGTGCACC	1163
950	Db	--AGGAACAATACCGATGTGTTCAACTGGGAAGGTGGGGCAGGCTCAGACAAACTGGGCA	1007
1164	Qy	AGTTGCTTGAGGGCAGCCTCCATTGCCAGATCATCATCAACAGCAATTCACACGATGAGG	1223
1008	Db	GCCTTCCC---ATCCCTGGCTGTGGCCCAAGATCATCATCTGTAATTCACACCCCATGTACC	1064
1224	Qy	AGGACGACTATGACATCGCCCTCATGCGGCTGTCCAAGCCCTTGACCCCTGTCCGCTCACA	1283
1065	Db	CCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTTCCCACCTCACTTTCTCAGGCACAG	1124
1284	Qy	TCCACCTCTGTGCTCTCCCATGATGGAACAGACTTGTAGCTCAATGAGACTGTCTGTGA	1343
1125	Db	TCAGGCCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGGCACACCCCACTCTGGA	1184
1344	Qy	TCACAGGCTTTGGCAAGACACGAGGAGACAGATGACAGACATCCCCCTTCCCTCCGGGAGG	1403
1185	Db	TCATTGGATGGGGCTTTACGAAGCAGAAATGGAGGGAAGATGTCTGACATACTGCTGCAGG	1244
1404	Qy	TGCAGGTCAATCTCATCGAATTCAAGAAATGCAATGACTACTTGGTCTATGACAGTTTACC	1463
1245	Db	CGTCAGTCTCAGGTCAATTGACAGCACACGGTGCATATGACAGATGCGTACAGGGGGAG	1304
1464	Qy	TTACCCCAAGATGATGTGTCTGGGACCTTTCGTGGGGCAGAGACTCTCTGCCAGGGAG	1523
1305	Db	TCACCGAAGAATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGAACACTGCCCAGGGTG	1364
1524	Qy	ACAGGGGGGGCCTTGTCTGTGTAGCAGAAACACCCGCTGGTACTCTGGCAGGTGTACCA	1583
1365	Db	ACAGTGTGTGGGCCCTGATGT---ACCAATCTGACAGTGGCATGTGTGTGGGCATTCGTTA	1421
1584	Qy	GCTGGGCAACAGGCTGTGGCCAGAGAAACAACTCTGTGTGTACACCAAAAGTGACAGAAG	1643
1422	Db	GCTGGGGCTATGGCTGTGGGGGCCCGAGCACCCACAGAGTATACACCAAGTCTCAGCCT	1481
1644	Qy	TTCTTCCCTGGATTATACGCAAGATGGAGCGAGGTGCGGATTCAGAAAAATCTCTAACCAAG	1703
1482	Db	ATCTCAACTGTGATCTAATAATCTGTGAAGGTGTAGCTGTAAATGTCTGTGCCCTTTTCAG	1541

```

RESULT 4
US-09-518-046-1
; Sequence 1, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 1
; LENGTH: 2413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 gene
; US-09-518-046-1

Query Match          10.4%; Score 181.2; DB 3; Length 2413;
Best Local Similarity 55.6%; Pred. No. 8,7e-36;
Matches 414; Conservative 0; Mismatches 318; Indels 12; Gaps 3;

QY 953 AGGGCCATGACCGGGCGGATGCTGGAGAGGGCGCTGGCTCGGATAGCAAGTGGCTTGG 1012
Db      |||||
QY 777 AGGGGCTACAGCTCAGCATCGTGGGTGGAACAATGCTCTTGTCTTCGAGTGGCCCTGG 836
Db      |||||
QY 1013 CAAGTGAGTCTGCACCTTGGCACCACCCACATCTGTGGAGGCGACGCTCATTCAGCGCCAG 1072
Db      |||||
QY 837 CAGGCCAGCGCTTCAGTTTCAGGGCTACCACTGTGTGGGGGGCTCTGTCTATCATCAGCCCCCTG 896
Db      |||||
QY 1073 TGGGTGCTCACTGCCGCCCACTGCTCTTCTGTGACCCGCGGAGAAGGTCTCTGGAGGGCTGG 1132
Db      |||||
QY 897 TGGATCATCATCTGCTGCACTGTGTATTATG-----ACTTGTATCTTCCCAAGTCATGG 950
Db      |||||
QY 1133 AAGGTGTAGCGGGCCACCAAGCAACTCTGCACACCTGTGCCTGTGAGCGACGCTCCATTGCGGAG 1192
Db      |||||
QY 951 ACCATCCAGGTGGTCTAGTTTCCCTGTTTGGACAATCCAGCCCCATCCCACTTGTGTGGAG 1010
Db      |||||
QY 1193 ATCA-----TCATCAACAGCAATTACACCGATGAGGAGGACGACTATGACATGCGCCCTCATG 1249
Db      |||||
QY 1011 AAGATTGTCTACACAGCAAGTACAAAGCCAAAGAGCTGGGCAATGACATCGCCCTTATG 1070
Db      |||||
QY 1250 CGGCTGTCCAAAGCCCTGACCCCTGTCGGCTTCATCATCCACCTGCTTGCCTCCCCATGCGAT 1309
Db      |||||
QY 1071 AAGCTGGCGGGCCACTCAGCTTCAATGAATAATGATCGAGCTGTGTGCTTGCCTTGCCTCACTCT 1130
Db      |||||
QY 1310 GGCAGACACCTTTTAGCTCTCAATGAGACCTGTGTGATCACAGGCTTTGGCAAGACCAAGGAG 1369
Db      |||||
QY 1131 GAAGAGAACTTCCCCGATGGAAAGTGTCTGGACGTTCAGGATGGGGGGCCACAGAGGAT 1190
Db      |||||
QY 1370 ACAGATGACAAGACATGCCCTTCTCTCGGAGAGGTGAGGTGCAATCTCATGCACTTCAAG 1429
Db      |||||
QY 1191 GGAGGTGAC---GCCCTCCCTGTCTCTGAACCAACGCGGCGCTGCTCTTGGATTTCCAAACAAG 1247
Db      |||||
QY 1430 AATATCAATGACTACTTGGTCTTATGACTTACTTACCTCCCAAGGATGATGTGCTGCTGGG 1489
Db      |||||
QY 1248 ATCTGCAACACAGGAGCGTGTACGTGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGC 1307
Db      |||||
QY 1490 GACTTCTGTGGGGCGAGAGACTCTCTGCGAGGAGACAGCGGGGGGCTCTTGTCTGTGAG 1549
Db      |||||
QY 1308 TACTGTAGCGGTGGCGTGAACAGCTGCCAGGGGGAAGCGGG-GGGCCCTTGTGTGTCAA 1367
Db      |||||
QY 1550 CAGAACAAACGCTGGTACTCTGGCAGGTGTCAACAGCTGGGGGCAAGGCTGTGGCCAGAGA 1609
Db      |||||
QY 1368 GAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACCAAGCTTTGGCATCGGCTCGCAGAGGTG 1427
Db      |||||
QY 1610 AACAACTTGGTGTGTACACCAAGTGTACAGAGTGTCTTCCCTGGATTTACAGCAAGATG 1669
Db      |||||
QY 1428 AACAGCTGGGTGTACACCGTGTCACTCTTCTGTGACTGGATCCACGAGCAGATG 1487
Db      |||||
QY 1670 GAGAGGAGGTGGATTCAGAAAA 1693
Db      |||||
QY 1488 GAGAGAGACTTAAAAACCTGAGA 1511
Db      |||||

RESULT 5
US-08-807-151-2
; Sequence 2, Application US/08807151
; Patent No. 6043033
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL HUMAN PROSTATIN-ASSOCIATED
; TITLE OF INVENTION: PROTEASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

```


QY	1029	TCGGCACCACCATCTGTGGAGGCACGCTCATTTGACGCCCAAGTGGGTGCTCACTGCCG	1088
DB	297	TCAGAAAGCTCCACGTTGCGGAGGCTCCATCATACCCCGAGTGGATCGTGACAGCG	356
QY	1089	CCCACTGCTCTTTCGTGACCCCGGAGAAAGTCTCTGAGGGCTCGAAGGTGTACGCGGCA	1148
DB	357	CCCACTGGGTGAAAACCTTTAACTCATTCATGGCATTTGACGGCATTTGGCGGGAATTT	416
QY	1149	CCAGCAACCTGCACCAAGTTGCGCTGAGGACGCTCCATGTCGGAGA--TCATCATCAACA	1205
DB	417	TGAGACAATCTTTCTATGTTCTATGGAGCGGATACCAAGTAGAAAAAGTGATTTCTCATC	476
QY	1206	GCAATTACACCGATGAGGAGGACGACTATGACATCGCCTCATGCGGCTGTCCAAGCCCC	1265
DB	477	CAAAATTATGACTCCAGACCAAGAACAAATGACATTTGGCTGATGAAGCTCCAGAGGCCTC	536
QY	1266	TGACCCCTGTCCGCTCACATCACCCCTCTTGGCCTCCCATGTCATGGACAGACCTTTAGCC	1325
DB	537	TGACTTTCAACGACCTAGTGAACCACTGTGTCTGCCCAACCCAGGCATGATGCTGCAGC	596
QY	1326	TCAATGAGACCTGTCTGGATCAGAGCTTTGGCAAGACCAAGGAGACAGATGACAAGACAT	1385
DB	597	CAGAAACAGCTCTGCTGATTTCCGGGTGGGGGGCCACCGAGGAGA---AAGGGAAGACCT	653
QY	1386	CCCCCTTCCTCGGAGGTGCAAGTCAATCTCATCGACTTCAAGAAATGCAATGACTACT	1445
DB	654	CAGAAAGTGTCTGAACGCTGCCAAGGTCTTCTCATTTGAGACACAGAGATGCAACAGCAGAT	713
QY	1446	TGGTCTATGACAGTTACTTACCCCAAGGATGATGTGTCTGGGGACCTTCGTGGGGGCA	1505
DB	714	ATGTCTATGACAACCTGATCACACCGCATGATCTGTGCGGCTTCTGCGAGGGAACG	773
QY	1506	GAGACTCTGCCAGGAGAGACAGCGGGGGGCTCTTGTCTGTGAGCAAAACAACGCTGGT	1565
DB	774	TCGATTTCTGCCAGGTGACAGTGGAGGGGCTTCTGGTCACTTCGAAAGAACTATCTGGT	833
QY	1566	ACTTGGCAGGTGTCAACAGCTGGGGCAACGCTGTGGCCAGAGNAACAACCTGGTGTGT	1625
DB	834	GGCTGATAGGGGATACAAAGCTGGGGTTCTGGCTGTGCCAAGCTTACAGACCCAGGAGTGT	893
QY	1626	ACACCAAGTGAACAGAAAGTTCTTCCCTGGATTTACAGCAAGATGGAGAGCGAGTGCAT	1685
DB	894	ACGGGATGTGATGGTATTCACGACTGGATTTATCGACAATAGAGGGCAGACGGCTAAT	953
QY	1686	TCGAAATACTCT	1697
DB	954	CCCATGGTCTT	965

RESULT 7

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US/09-342-749-1
; Sequence 1, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-P.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: IMPRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 60/091,044
; EARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

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1004 CAAATATGACTCCAGAACAGAAACAATGACATTTGGCTGATGAAGCTGCAGAGCCCTC 1063
1266 TGACCCCTGTCGCTCAGATCCACCTCTGCTCCCTCCCATGCTGATGACAGACCTTTAGCC 1325
1064 TGACTTTCAACGACCTAGTGAACACCAAGTGTCTGCTCCCAACCCAGGATGATGCTGAGC 1123
1326 TCAATGAGACCTGCTGATCAGAGCTTTGGCAAGACCCAGGAGACAGATGACAAGACAT 1385
1124 CAGAACAGCTCTGCTGATTTCCGGTGGGGGCCACCGAGAGA---AAGGGAAGACCT 1180
1386 CCCCCTTCCTCCGGAGGTGAGTCAATCTCATGCTGCTTCAAGAAATGCAATGACTACT 1445
1181 CAGAAGTGTGACCTGCAAGCTGCAAGTGTCTTCTCATTTGAGACACAGAGATGCAACAGCAGAT 1240
1446 TGGTCTATGACAGTTACTTACCCCAAGGATGATGTGCTGGGACCTTCTGTTGGGGGCA 1505
1241 ATGCTATGACAACTGATACACAGGCATGATCTGTGCGGGTCTCTGAGGGGAGCG 1300
1506 GAGACTCTGTCAGGAGAGACAGCGGGGGCTCTTGTCTGTGAGCAGAAACAACTGCTGT 1625
1301 TCGATTCTTCCAGGGTGACAGTGGAGGGCTCTGCTCACTTCGAAGAAACAATATCTGGT 1360
1566 ACCTGGAGGTGTCAACAGCTGGGACAGAGCTGTGGCAGAGAAACAACTGCTGT 1625
1361 GGCTGATAGGGGATACAGCTGGGGTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1420
1626 ACACCAAGTACAGAAAGTCTTCTCCCTGATTTACAGCAAGATGAGAGCGAGG 1679
1421 ACGGAATGTATGATGATTTACAGGACTGATTTATCGAATGAGGCGAGCG 1474

RESULT 8

US-09-691-840-1
; Sequence 1, Application US/09691840
; Patent No. 644419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: THPRS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1476)
; NAME/KEY: conflict
; LOCATION: (724)
; OTHER INFORMATION: Listed as T in GenBank Accession No. U75329
; NAME/KEY: conflict
; LOCATION: (985)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
; NAME/KEY: conflict
; LOCATION: (1347)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
; NAME/KEY: conflict
; LOCATION: (1466)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329
; NAME/KEY: conflict
; LOCATION: (1471)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329.
; NAME/KEY: allele

LOCATION: (478)
; OTHER INFORMATION: This base can be G or A with G being the more
; OTHER INFORMATION: common allele. The codon will change from Val to
; OTHER INFORMATION: Met.
; NAME/KEY: allele
; LOCATION: (777)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. The codon is unaffected with both
; OTHER INFORMATION: alleles encoding Gly.
; NAME/KEY: allele
; LOCATION: (768)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.
; NAME/KEY: allele
; LOCATION: (834)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.
; NAME/KEY: allele
; LOCATION: (625)
; OTHER INFORMATION: This base can be T or A with T being the more
; OTHER INFORMATION: common allele. The codon will change from Phe to Ile
; US-09-691-840-1

Query Match 10.1%; Score 176.4; DB 4; Length 1479;
Best Local Similarity 54.9%; Pred. No. 1.1e-34;
Matches 392; Conservative 0; Mismatches 316; Indels 6; Gaps 2;
QY 969 GGATCGTGGAGGGCGCTGCGCTCGGATAGCAGTGGCTTGGCAAGTGAAGTCTGCACT 1028
DB 764 GGATCGTGGAGGGCGGAGAGCGCGCTCCCGGGGGCTGCGCTGCGAGTCAAGCTGCAAG 823
QY 1029 TCGGCACACCCACATCTGTGGAGGACGCTCATATGAGCCCGAGTGGTGTCTCATGCGG 1088
DB 824 TCCAGAAAGTCCAGTGTGCGAGGCTCCATCATACCCCGAGTGGATCTGACAGCGG 883
QY 1089 CCCACTGCTTCTTCTGTCGACCCCGGAGAGGCTCCTGAGGGCTGGAAGTGTACGCGGCA 1148
DB 884 CCCACTGCTGGAAGAACCTCTTAACAATTCATGGCATTTGACCGCATTTGCGGGGATTT 943
QY 1149 CCAGCAACCTGCACACAGTTGCTTGAGGAGCGCTCCATTTGCCGAGA---TCATCATCAACA 1205
DB 944 TGAGACATCTTTTATGTTCTATGAGCGGATACCAAGTAGAAGAAAGTATTTCTCATC 1003
QY 1206 GCAATTACCGATGAGAGAGACGATATGACATGCGCTCATGCGGCTGTCCAAAGCC 1265
DB 1004 CAAATTATGACTCCAGAACCAAGAAATGATGATGCTGATGAAGCTGCAAGAGCCTC 1063
QY 1266 TGACCTGTCGCTCAGATCCACCTGCTGCTCCCATGCTGCTGCTGCTGCTGCTGCTGCTG 1325
DB 1064 TGACTTTCAACGACCTAGTGAACCAAGTGTCTGCTCCCAACCCAGGATGATGCTGAGC 1123
QY 1326 TCAATGAGACCTGCTGATCAAGCTTTGGCAAGACCCAGGAGACAGATGACAAGACAT 1385
DB 1124 CAGAACAGCTCTGCTGATTTCCGGTGGGGGCCACCGAGAGA---AAGGGAAGACCT 1180
QY 1386 CCCCCTTCCTCCGGAGGTGAGTCAATCTCATGCTGCTTCAAGAAATGCAATGACTACT 1445
DB 1181 CAGAAGTGTGCAAGCTGCAAGTGTCTTCTCATTTGAGACACAGAGATGCAACAGCAGAT 1240
QY 1446 TGGTCTATGACAGTTACTTACCCCAAGGATGATGTGCTGGGACCTTCTGTTGGGGGCA 1505
DB 1241 ATGCTATGACAACTGATCAACAGGCATGATCTGTGCGGGTCTCTGAGGGGAGCG 1300
QY 1506 GAGACTCTGCGAGGAGACAGCGGGGGCTCTTGTCTGTGAGCAGAAACAACTGCTGT 1565
DB 1301 TCGATTCTTCCAGGGTGACAGTGGAGGGCTCTGCTCACTTCGAAGAAACAATATCTGGT 1360
QY 1566 ACCTGGAGGTGTCAACAGCTGGGACAGAGCTGTGGCAGAGAAACAACTGCTGT 1625
DB 1361 GGCTGATAGGGGATACAGCTGGGGTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1420
QY 1626 ACACCAAGTACAGAAAGTCTTCTCCCTGATTTACAGCAAGATGAGAGCGAGG 1679

Db 1421 ACGGGAATGTGATGTTATTCACGGACTGGATTTATCGACAAATGAGGGCAGACG 1474

RESULT 9
US-09-342-749-29
; Sequence 29, Application US/09342749
; Patent No. 6156194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; EARLIER FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 60/091,044
; EARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 2479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-342-749-29

Query Match 10.0%; Score 175.6; DB 3; Length 2479;
Best Local Similarity 54.4%; Pred. No. 2.2e-34;
Matches 398; Conservative 0; Mismatches 328; Indels 6; Gaps 2;

QY 969 GGATCGTGGAGGGCGCTGGCTCGGATAGCAAGTGGCTTCGCAAGTGAAGTCTGCACCT 1028
DB 820 GGATCGTGGAGGGCGCTGGCTCGGAGCGCGCTCCCGGGGGCTTGGCTTCGCAAGTGAAGTCTGCACG 879

QY 1029 TCGGCACCAACCCACATCTGTGGAGGCAAGCTCTATGACGCCAGTGGTGTCTCACTGCCG 1088
DB 880 TCAGAACGTCACAGTGTGGAGGCTCCATCATCATCCCCGAGTGGATGTGTCACAGCG 939

QY 1089 CCACCTGCTTCTTCGTGACCCGGGAGAGGTCTCTGGAGGCTGGAAGGTGTACGCGGCA 1148
DB 940 CCACCTGCTGGAACCACTCTTAACAAATCATGGCATTTGGACGGCATTTGGCGGGATTT 999

QY 1149 CAGCAACCTGCACAGTTCCTTGGAGCGAGCTCCATTCGCGAGA---TCATCATCAACA 1205
DB 1000 TGAGACAAATCTTTTCATGTTCTATGGAGCGGATACCAAGTACAAAAGTATTTCTCATC 1059

QY 1206 GCAATTACACCGATGAGGAGGACGATGACATTCGCGCTTCATCGCGCTCTCCAAGCCCC 1265
DB 1060 CAAATTATGACTCCAGAACCAAGAAACAAATGACATTTGGCTGTATGAAGTCTGCAGAGCCTC 1119

QY 1266 TGACCTGTCCGCTCATCATCCACCTGCTTGGCTCCCATGCGATGGACAGACCTTTAGCC 1325
DB 1120 TGACTTTCAACGACCTAGTGAACCAAGTGTGTCTGCCCAACCCAGGCAATGCTGCAGC 1179

QY 1326 TCAATGAGACCTGCTCGATCAGAGGCTTTGGCAAGACCAAGGAGACAGATGACAGACAT 1385
DB 1180 CAGAACAGCTCTGCTGATTTCCGGTGGGGGGCCACCGAGGAGA---AAGGGAAGACCT 1236

QY 1386 CCCCCCTTCTCCGGAGGTCAGGTCAATCTCATTCGACTTCAAGAAATGCAATGACTACT 1445
DB 1237 CAGAAAGTGTGAAACGCTGCGCAAGGTGCTTCTCATTTGAGACACAGATGCAACAGCAGAT 1296

QY 1446 TGGTCTATGACAGTACCTTACCCCAAGGATGATGTGCTGGGGACCTTCGTGGGGCA 1505
DB 1297 ATGTCTATGACAACCTGATCACAACCCAGCCTATGATCTGTGCGGGCTTCCTGAGGGGAACG 1356

QY 1506 GAGACTCTCCAGGAGGACAGCGGGGGCTCTTGTCTGTGAGCGAGCAACAACCGCTGTT 1565
DB 1357 TCGATTCTTCCAGGTTGACAGTGGAGGGCTCTGTGTCATCTTCAACAAATATCTGTT 1416

QY 1566 ACTTGGCAGGTGTCAACAGCTGGGGCACAAGGCTGTGGCCAGAGAAACAAACCTGTTGTGT 1625
DB 1417 GGCTGATAGGGGATACAAGCTGGGGTTCGCTGTGCCAAGCTTACAGACCAAGGAGTGT 1476

QY 1626 ACACCAAGTGCACAGAGTTCCTCCCTGATTTTACAGCAGATGGAGAGCGAGTGGCAT 1685
DB 1477 ACGGGAATGTGATGTTATTCACGGACTGGATTTATCGACAAATGAGGGCAACCGGTAAT 1536

QY 1686 TCAGAAAATCCT 1697
DB 1537 CCATATGGTCTT 1548

RESULT 10
US-09-691-840-29
; Sequence 29, Application US/09691840
; Patent No. 644419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 2479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-691-840-29

Query Match 10.0%; Score 175.6; DB 4; Length 2479;
Best Local Similarity 54.4%; Pred. No. 2.2e-34;
Matches 398; Conservative 0; Mismatches 328; Indels 6; Gaps 2;

QY 969 GGATCGTGGAGGGCGCTGGCTCGGATAGCAAGTGGCTTCGCAAGTGAAGTCTGCACCT 1028
DB 820 GGATCGTGGAGGGCGCTGGCTCGGAGCGCGCTCCCGGGGGCTTGGCTTCGCAAGTGAAGTCTGCACG 879

QY 1029 TCGGCACCAACCCACATCTGTGGAGGCAAGCTCTATGACGCCAGTGGTGTCTCACTGCCG 1088
DB 880 TCAGAACGTCACAGTGTGGAGGCTCCATCATCATCCCCGAGTGGATGTGTCACAGCG 939

QY 1089 CCACCTGCTTCTTCGTGACCCGGGAGAGGTCTCTGGAGGCTGGAAGGTGTACGCGGCA 1148
DB 940 CCACCTGCTGGAACCACTCTTAACAAATCATGGCATTTGGACGGCATTTGGCGGGATTT 999

QY 1149 CAGCAACCTGCACAGTTCCTTGGAGCGAGCTCCATTCGCGAGA---TCATCATCAACA 1205
DB 1000 TGAGACAAATCTTTTCATGTTCTATGGAGCGGATACCAAGTACAAAAGTATTTCTCATC 1059

QY 1206 GCAATTACACCGATGAGGAGGACGATGACATTCGCGCTTCATCGCGCTCTCCAAGCCCC 1265
DB 1060 CAAATTATGACTCCAGAACCAAGAAACAAATGACATTTGGCTGTATGAAGTCTGCAGAGCCTC 1119

QY 1266 TGACCTGTCCGCTCATCATCCACCTGCTTGGCTCCCATGCGATGGACAGACCTTTAGCC 1325
DB 1120 TGACTTTCAACGACCTAGTGAACCAAGTGTGTCTGCCCAACCCAGGCAATGCTGCAGC 1179

QY 1326 TCAATGAGACCTGCTCGATCAGAGGCTTTGGCAAGACCAAGGAGACAGATGACAGACAT 1385
DB 1180 CAGAACAGCTCTGCTGATTTCCGGTGGGGGGCCACCGAGGAGA---AAGGGAAGACCT 1236

QY 1386 CCCCCCTTCTCCGGAGGTCAGGTCAATCTCATTCGACTTCAAGAAATGCAATGACTACT 1445
DB 1237 CAGAAAGTGTGAAACGCTGCGCAAGGTGCTTCTCATTTGAGACACAGATGCAACAGCAGAT 1296

QY 1446 TGGTCTATGACAGTACCTTACCCCAAGGATGATGTGCTGGGGACCTTCGTGGGGCA 1505
DB 1297 ATGTCTATGACAACCTGATCACAACCCAGCCTATGATCTGTGCGGGCTTCCTGAGGGGAACG 1356

QY 1506 GAGACTCTCCAGGAGGACAGCGGGGGCTCTTGTCTGTGAGCGAGCAACAACCGCTGTT 1565
DB 1357 TCGATTCTTCCAGGTTGACAGTGGAGGGCTCTGTGTCATCTTCAACAAATATCTGTT 1416

QY 1566 ACTTGGCAGGTGTCAACAGCTGGGGCACAAGGCTGTGGCCAGAGAAACAAACCTGTTGTGT 1625
DB 1417 GGCTGATAGGGGATACAAGCTGGGGTTCGCTGTGCCAAGCTTACAGACCAAGGAGTGT 1476

Db 1297 ATGTCTATGACAAACCTGATCACACACAGCCATGATCTGTGCCGGCTTCTTCGACGGGAACG 1356
Qy 1506 GAGACTCTCCAGGAGACAGCGGGGGCTCTTGTCTGTGAGCAGAACAAACCGCTGGT 1565
Db 1357 TCATCTTCCAGGGGTGACAGTGGAGGGCTCTGGTCACTTGAACAAATATCTGGT 1416
Qy 1566 ACCTGGCAGGTGTACACAGCTGGGGCAAGGCTGTGGCCAGAGAAACAAACCTGGTGTGT 1625
Db 1417 GGCTGATAGGGGATACAAAGCTGGGGTCTGGCTGTGCCAAAGCTTACAGACCAAGAGTGT 1476
Qy 1626 ACACCAAGTGACAGAAGTCTTCCCTGGATTATACAGAGATGAGAGCGAGTGGAT 1685
Db 1477 ACGGGAATGTGATGTATTACCGACTGGATTTATCGACAAATGAAGGCAACCGCTAAT 1536
Qy 1686 TCAGAAATCT 1697
Db 1537 CCACATGGTCTT 1548

RESULT 11

US-09-261-416-1
; Sequence 1, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12 J. No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 144..1511
; OTHER INFORMATION: CDS
US-09-261-416-1

Query Match 9.1%; Score 158.2; DB 3; Length 2416;

Best Local Similarity 55.4%; Pred. No. 4.8e-30; Mismatches 318; Indels 15; Gaps 5;

Matches 414; Conservative 0; Mismatches 318; Indels 15; Gaps 5;

Qy 953 AGGGCCATGACCGGGCGGATCGTGGAGGGGGCGCTGGCTCGGATAGCAAGTGGCTTGG 1012

Db 777 AGGGCTACAGTCAAGCATCGTGGTGGAAACATGTCCTTGTCTCGCAGTGGCCCTGG 836

Qy 1013 CAAGTGATCTGACTTCGGCACCAACCATCTGTGGAGGACGCTCATTTGACGCCCGAG 1072

Db 837 CAGGCCAGCCTTCAGTTCAGGGCTACCACTGTGGGGGGCTCTGTCTATCACGCCCTGT 896

Qy 1073 TGGTGTCTCACTCGCGGCCACTGTCTTCTGTGACCGGGAGAGGTCCTGGAGGGCTGG 1132

Db 897 TGGATCATCATCTGTGCACATCTGTTATG-----ACTTGTACTCCCAAGTCAAG 950

Qy 1133 AAGGTGTAGCGGGGACCCAGCAACCTGCACAGTTGCTGTGAGGAGCCTCCATTCGCCAG 1192

Db 951 ACCATCCAGGTGGGTCTAGTTTCCCTGTGTGACAAATCCAGCCCCATCCACTTGTGGAG 1010

Qy 1193 ATCATCAT---CAACAGCAATTTACCCGATGAGGAGGACGACTATGACATGCCCTCATG 1249

Db 1011 AAGATTGTTTACCAAGCAAGTACCAAGCCAAAGAGGCTGGGCAATGACATGCCCTTATG 1070

Qy 1250 CGGTGTCCAAAGCCCTGACCTGTCCGCTCACATCCACCTGTGCTTCCCTCCCATGCAT 1309

Db 1071 AAGTGGCGGGGCACTCAGCTTCAATGAATGATCCAGCTGTGTGCTGCTGCCAACTCT 1130

Qy 1310 GGACAGACTTTCAGCTCAATGAGACCTGCTGGATCACAGGCTTTGGCAAGCCAGGAG 1369

Db 1131 GAAGAGAACTTCCCGGATGGAAAGTGTGCTGGACGTGAGGATGGGGGGCCACAGAGGAT 1190

Qy 1370 ACAGATGACAAAGACATCCCCCTTCTCTCGGAGAGGTGAGGTCAATCTCATGACTTC-AA 1428
Db 1191 GGAGGTGAC---GCCTCCCCCTGCTCTGAACACACGCGGCCCTCCCTTTGATTTCCAAACA 1247
Qy 1429 GAAATGCAATGACTACTTGTCTATGACAGTTACTTTACCCCAAGGATGATGTGCTGG 1488
Db 1248 GATCTGCAACCAACAGGACGTGTACGTTGACATCACTCCCTCCATGCTCTGCGGGG 1307
Qy 1489 GGAACCTTCTGTGGGGG---AGAGACTCTCTGCGAGGACACAGCGGGGGGCTCTTGTCTGT 1546
Db 1308 CTACTGACGGGTGGGTTGGAACACAGCTGCGAGGGGACAGCGGGGGGCTCTGTTGTGT 1367
Qy 1547 GAGCAGAAACACCGCTGTGTTACTTGGCAGGTGTACAGCTGGGGGACAGGCTGTGGCCAG 1606
Db 1368 CAAGAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACCAAGCTTTGGCATCGGCTGCCAGAC 1427
Qy 1607 AGAAACAAACCTGTGTGTACACCAAGATGACAGAGTCTTCTCCCTGGATTTACAGCAAG 1666
Db 1428 GTGAACCAAGCCTGGGGGTGTACACCCGTGTCACTCTTCTGGACTGGATCCAGGACG 1487
Qy 1667 ATGGAGAGCGAGGTGCGATTTCAGAAAA 1693
Db 1488 ATGGAGAGAGACCTAAAAACCTGAAGA 1514

RESULT 12

US-09-518-046-3
; Sequence 3, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 3
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 variant gene
US-09-518-046-3

Query Match 8.8%; Score 154.2; DB 3; Length 2544;

Best Local Similarity 58.1%; Pred. No. 4.9e-29;

Matches 292; Conservative 0; Mismatches 208; Indels 3; Gaps 1;

Qy 1191 AGATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATGCCCTCATGC 1250

Db 1143 AGATTGTCTACACAGCAAGTACAGCCAAAGAGCTGGGCAATGACATGCCCTTATGA 1202

Qy 1251 GGCTGTCCAAAGCCCTGACCCCTGTCCGCTCACTCCACCTCTTGTGCTCCCAATGCATG 1310

Db 1203 AGCTGGCGGGCCACTCAGTTCATGAATGATCCAGCCTGTGTGCTGCCCACTCTG 1262

Qy 1311 GACAGACTTTAGCCTCAATGAGACCTGTGTGATCAAGGCTTTGGCAAGACGAGGAGA 1370

Db 1263 AAGAGAACTTCCCGGATGGAAAGTGTCTGAGACTCAGGATGGGGGGCCACAGAGGATG 1322

Qy 1371 CAGATGACAGACATCCCCCTTCTCCGAGAGGTGACGTCATCTCATGACTTCAAGA 1430

Db 1323 GAGGTGAC---GCCTCCCCCTGTCTGAAACACAGCGGGCGCTCCCTTTGATTTCCAAACA 1379

Qy 1431 AATCAATGACTACTTGTCTATGACAGTTTACCTTTACCCCAAGGATGATGTGTCTGGGG 1490

Db 1380 TCTGCAACCAAGGAGCGTGTACGGTGGCATCACTCCCTCCCTCCATGCTCTGCGCGGCT 1439

QY 1491 ACCTTGTGGGCGAGAGACTCTGCGGAGAGACAGGGGGGCTCTTGTCTGTGAGC 1550
Db 1440 ACCTGACGGGTGGCGTGAGCAGCTGCGGAGGAGACAGGGGGGCTCTTGTGTCAAG 1499
QY 1551 AGAACAAACCGCTGTACTCTGGCAGGTGTACACAGCTGGGCGACAGGGCTGTGGCCAGAGAA 1610
Db 1500 AGAGGAGGCTGTGGAAGTTAGTGGAGGACAGCTTTGGCATCGGCTGGCGAGGTGA 1559
QY 1611 ACAACCTGTGTGTACACCAAGATGACAGAAAGTTCTTCCCTGGAATTTACAGCAAGATGG 1670
Db 1560 ACAAGCCTGGGGTGTACACCGGTGTACCTCTTCTCGGAGCTGTATCCACGAGCATGG 1619
QY 1671 AGAGCGAGTGGCATTCAGAAA 1693
Db 1620 AGAGAGACCTAAACCTGAAGA 1642

RESULT 13

US-09-510-738A-188
; Sequence 188, Application US/09510738A
; Patent No. 6268165
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A
; CURRENT APPLICATION NUMBER: US/09/510,738A
; PRIOR FILING DATE: 2000-02-22
; PRIOR FILING DATE: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 188

; LENGTH: 1783

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: full length cDNA of hepsin

US-09-510-738A-188

Query Match 8.5%; Score 148.4; DB 3; Length 1783;
Best Local Similarity 53.3%; Pred. No. 1.2e-27;
Matches 448; Conservative 0; Mismatches 356; Indels 36; Gaps 5;

QY 867 ACAATCCACATCCAGGAAGCTCCACAGTCTGAATGCCCTTCCAGCGGTATATCT 926
Db 625 ACACCGAGGCTGCTGGAGTCACTCCGCTGTGATTCGCCCCAGAGCGCTTCTTGG 684
QY 927 CCTCCAGTCTTCCACTCGGACTGAGGGCCATGACCGGG---CGGATCGTGGAGGG 983
Db 685 CCGCATCTCCAGACTGTGGCGGAGAGCTGCCCGTGGACCGCATCTGGAGGCC 744
QY 984 CGTGGCTCGGATAGCAAGTGGCTTGGCAAGTGTGCACTTGGCACCACCCACA 1043
Db 745 GGGACACCACTTGGGCGGCTGGCGGCAAGTCAAGCTTCGCTATGATGGAGCAC 804
QY 1044 TCTGTGGAGCAGCTATTGAGCCAGTGGTGTCTCACTGGCCGCTTCTTC--- 1099
Db 805 TCTGTGGGATCCCTGCTCTCGGGACTGGGTGTGACAGCGGCCCTCTTCCCG 864
QY 1100 -----TTCTGTGACCCGGAGAGGTCTCTGGAGGCTGGAAGGTGTACGCGGCA 1148
Db 865 AGCGGAACCGGTCTCTCCGATGGCGAGTGTTCGCGTGGCGGCGGCTCTC 924
QY 1149 CAGCAACCTGACAGTGTGCTGAGGCGAGCTTCATTTGGCCGAGATCATCAACAGCA 1208
Db 925 CCGAGCTCTGACGTGGGGGTGACGCTGTGTCTTACACGGGGCTATCTTCCCTTC 984
QY 1209 ATTACACCGAT---GAGGAGGAGCTATCATCTCCCTCATCGGCTGTCCAGCC 1265
Db 985 GGGACCCCAACAGCGAGGAGACAGCAACATATGCTCTGGTCCACCTCTCCAGTCCC 1044
QY 1266 TGACCTGTCTCGCTCAATCCACCTGCTGCTCCCATGTCATGACAGACCTTTAGCC 1325

Db 1045 TGGCCCTCAGAGATATCATCCAGCTGTGTGCTCCAGCTGCGGCGAGGCCCTGTGG 1104
QY 1326 TCAATGAGACTCTGTGATCAGAGGCTTTGGCAAGACCGAGGAGACAGATGCAAGACAT 1385
Db 1105 ATGCGAAGATCTGTACCGTACGGCTGGGGCAA---CAGCAGTACTATGGCCACAGG 1161
QY 1386 CCCCCTTCTCCGGAGGTGCAAGTCAATCTCATGCACTTCAAGAAATGCAATGACTACT 1445
Db 1162 CCGGGGTACTCCAGGAGCTCGAGTCCCAATATCAGCAATGATGTCTGCAATGGCGCTG 1221
QY 1446 TGGTCTATGACAGTTACTTACCCCAAGGATGTGTGCTGGGAGCTTCTGTGGGCA 1505
Db 1222 ACTTCTATGGAACACGATCAGCCCAAGATTTCTGTGTGCTACCCGAGGTGCA 1281
QY 1506 GAGACTCTCCCGAGGAGACAGCGGGGGCTCTTGTCTGTGAGCAGAACAC--- 1558
Db 1282 TTGATGCTCCAGGGCGACAGCGGTGTCCTTTGTGTGTGAGGACAGCATCTCTCGA 1341
QY 1559 -----CGCTGTACTTGGCAGGTGTACAGCTGGGGCAGAGGTGTGGCCAGAGAAC 1613
Db 1342 CGCCACGTTGGCGGCTGTGTGGCAATTGTGAGTTGGGGCACTGGCTGTGCCCTGCCAGA 1401
QY 1614 AACTGTGTGTACACCAAGTGCAGAGTCTTCTCCCTGATTTACAGCAAGATGAGA 1673
Db 1402 AGCAGCGCTTAACCAAGTCACTGACTTCCGGAGTGTGATCTTCCAGGCCATAAGA 1461

RESULT 14

US-09-861-966-188
; Sequence 188, Application US/09861966
; Patent No. 8518028
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A/Div
; CURRENT APPLICATION NUMBER: US/09/861,966
; PRIOR FILING DATE: 2001-05-21
; PRIOR FILING DATE: 09/510,738
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 188

; LENGTH: 1783

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: full length cDNA of hepsin

US-09-861-966-188

Query Match 8.5%; Score 148.4; DB 4; Length 1783;
Best Local Similarity 53.3%; Pred. No. 1.2e-27;
Matches 448; Conservative 0; Mismatches 356; Indels 36; Gaps 5;

QY 867 ACAATCCACATCCAGGAAGCTCCACAGTCTGAATGCCCTTCCAGCGGTATATCT 926
Db 625 ACACCGAGGCTGCTGGAGTCACTCCGCTGTGATTCGCCCCAGAGCGCTTCTTGG 684
QY 927 CCTCCAGTCTTCCACTCGGACTGAGGGCCATGACCGGG---CGGATCGTGGAGGG 983
Db 685 CCGCATCTGCCAAGACTGTGGCGGAGAGTGTCCCGTGGACCGCATCTGGAGGCC 744
QY 984 CGTGGCTCGGATAGCAAGTGGCTTGGCAAGTGTGCACTTGGCACCACCCACA 1043
Db 745 GGGACACCACTTGGGCGGCTGGCGGCAAGTCAAGCTTCGCTATGATGGAGCAC 804
QY 1044 TCTGTGGAGCAGCTCATTTGAGCCAGTGGTGTCTCACTGGCCGCTTCTTC--- 1099
Db 805 TCTGTGGGATCCCTGCTCTCCGGGACTGGGTGTGACAGCGGCCCTCTTCCCG 864
QY 1100 -----TTCTGTGACCCGGAGAGCTCTCTGAGGCTGGAAGGTGTACCGGGCA 1148
Db 865 AGCGGAACCGGTCTCTCCGATGGCGAGTGTTCGCGTGGCGGCGGCTCTC 924

QY 1149 CCAGCAACCTGCGACGAGTTCCTGAGGAGCCCTCCATTGCGGAGATCATCATCAACAGCA 1208
Db 925 CCCACGCTCTGAGCTGGGGGTGACGGCTGTGTCTACCAAGGGGGTATCTTCCCTTTC 984
QY 1209 ATTACACCGAT---GAGGAGGACGACTATGACATGCGCCCTCATGCGGCTGTCCAGGCC 1265
Db 985 GGGACCCCAACAGCGAGGAGAAAGCAACGATATGCGCCCTGGTCCACCTCTCCAGTCCCC 1044
QY 1266 TGACCCCTGTCGCTCATCATCCACCTGCTTTCCTCCCATGTCATGAGACAGACCTTTAGCC 1325
Db 1045 TGCCCTTCAAGATATCATCCAGCTGTGTGCTCCAGCTGCGGCGAGGCCCTGTGG 1104
QY 1326 TCAATGAGACTGCTGATCAGAGCTTTGGGAGACCAAGGAGACAGATGACAGACAT 1385
Db 1105 ATGCAAGATCTGTACCGTACGCGGCTGGGGCAA---CACGCACTACTATGCGCAACAGG 1161
QY 1386 CCCCCTTCCTCGGGAGGTGAGTCAATCTCATGACTTTCAGAAATGCAATGACTACT 1445
Db 1162 CCGGGGTACTCCAGAGGCTCGAGTCCCCATAATCAGCAATGATGTCTGCAATGGCCGTG 1221
QY 1446 TGCTCTATGACAGTTACTTACCCCAAGAGTGTGTGCTGGGAGCTTTCGTGGGGCA 1505
Db 1222 ACTTCTATGAAACAGATCAAGCCCAAGATGTTCTGTGCTGGTACCCCGAGGGTGGCA 1281
QY 1506 GAGACTCTGCGAGGAGACAGCGGGGGCTCTTGTCTGTGAGCAGAACAC----- 1558
Db 1282 TTGATGCTGCGAGGGGACAGCGGTGTGCTTGTGTGTGAGGACAGCATCTCTCGGA 1341
QY 1559 -----CGCTGCTACTGCGAGGTCTACCAAGTGGGACAGAGCTGTGGGCAAGAAC 1613
Db 1342 CGCCACGTTGGCGCTGTGTGGCAATTGTGAGTTGGGACATGGCTGTGCTGGCCAGA 1401
QY 1614 AACCTGTGTGTACCAAAAGTGCAGAGTTCTTCCCTGGATTTCAGCAAGATGAGA 1673
Db 1402 AGCCAGGCGTCTACCAAAAGTGCAGTGTCTCCGGAGTGGATCTTCAGGCCATAAGA 1461

RESULT 15
US-09-742-703-3
; Sequence 3, Application US/09742703
; Patent No. 6423543
; GENERAL INFORMATION:
; APPLICANT: Patrick Allen Marcotte
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEP5IN EXPRESSION
; FILE REFERENCE: RTS-0090
; CURRENT APPLICATION NUMBER: US/09/742,703
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (826)..(2079)
US-09-742-703-3

Query Match 8.5%; Score 148.4; DB 4; Length 2363;
Best Local Similarity 53.3%; Pred. No. 1.3e-27;
Matches 448; Conservative 0; Mismatches 356; Indels 36; Gaps 5;
QY 867 ACACTCCACCATCCAGAAAGCTTCCAGAGTCTGAATGCTTCCAGCGGTATATCT 926
Db 1205 ACACCCAGAGGCTGTGAGGTCTATCTCCGTGTGTGATTGCCCCCAGAGGCGGTTTCTGG 1264
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Job time : 136 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 17, 2003, 20:22:02 ; Search time 457 Seconds

(without alignments)
4097.808 Million cell updates/sec

Title: US-09-879-792-12

Perfect score: 2999

Sequence: 1 MERDSHGASPARTPSAGAS.....TEVLPWYXMSSEVRFKRS 562

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Searched:

2211378 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bite -START=1 -END=1 -MATRIX=bluelum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=ptc -THR MAX=100
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Database :

Published Applications NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	2999	100.0	1748	9	US-09-879-792-11	Sequence 11, Appl
2	2956	98.6	2393	13	US-10-353-690-99	Sequence 99, Appl
3	2775.5	92.5	1614	9	US-09-888-615-45	Sequence 1, Appl
4	2291.5	76.4	1434	15	US-10-177-661-1	Sequence 14, Appl
5	2287	76.3	1314	11	US-09-898-837A-14	Sequence 17, Appl
6	2287	76.3	1314	11	US-09-898-837A-17	Sequence 3, Appl
7	2108	70.3	1341	15	US-10-177-661-3	Sequence 16, Appl
8	1869	62.3	1078	11	US-09-898-837A-16	Sequence 35, Appl
9	1855	61.9	1230	9	US-09-879-792-35	Sequence 5, Appl
10	1436	47.9	1222	9	US-09-804-156-5	Sequence 3, Appl
11	1436	47.9	1222	13	US-10-319-519-5	Sequence 5, Appl
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13	1436	47.9	1222	14	US-10-125-459-3	Sequence 5, Appl
14	1436	47.9	1222	14	US-10-067-761-5	Sequence 28, Appl
15	1282.5	42.8	834	9	US-09-879-792-28	Sequence 30, Appl
16	893	29.8	678	9	US-09-879-792-30	Sequence 33, Appl
17	845.5	28.2	614	9	US-09-879-792-33	Sequence 6, Appl
18	785.5	26.2	3298	15	US-10-235-699-6	Sequence 22, Appl
19	745.5	24.9	2486	10	US-09-981-353-22	Sequence 5, Appl
20	743	24.8	3244	13	US-10-334-038-5	Sequence 929, App
21	743	24.8	3245	9	US-09-759-143-929	Sequence 929, App
22	743	24.8	3245	9	US-09-780-669-929	Sequence 929, App
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ALIGNMENTS

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; Sequence 11, Application US/09879792
; Patent No. US20020061850A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; APPLICANT: Gedrich, Richard
; TITLE OF INVENTION: Regulation of Human Transmembrane Serine
; TITLE OF INVENTION: Protease
; FILE REFERENCE: 02973.00035
; CURRENT APPLICATION NUMBER: US/09/879,792
; CURRENT FILING DATE: 2001-06-13
; PRIOR FILING DATE: 2001-06-13
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/211,224
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,353
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1748

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Qy 521 AlaGlyValThrSerTyrGlyThrGlyCysGlyGlnArgAsnLysProGlyValTyrThr 540
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; Sequence 45, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:

; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHITE, DAVID
; APPLICANT: CAENEPEL, SEAN
; APPLICANT: CHARIDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-888-615-45

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Qy 271 GluValAlaHisArgAspPheAlaAsnSerPheSerIleLeuArgTyrAsnSerThrIle 290
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; Publication No. US20030082783A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Virca, G. Duke
; TITLE OF INVENTION: DENDRITIC CELL TRANSMEMBRANE SERINE PROTEASE
; FILE REFERENCE: 3256-A
; CURRENT APPLICATION NUMBER: US/10/177,661
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/299,606
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1434
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1434)
; OTHER INFORMATION:
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Best Local Similarity: 95.71% Mismatches: 12
Query Match: 76.41% Indels: 3
DB: 15 Gaps: 1

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QY 440 AsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThrAspLysThrSer 459
Db 1063 AATGAGACCTGCTGGATCAGAGGCTTTGGCAAGACCAGGAGACAGATGACAGACATCC 1122
QY 460 ProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAspTyrLeu 479
Db 1123 CCTTCTCTCCGGAGGTGAGGTCAATCTCATCGACTTCAAGAAATGCAATGACTACTTG 1182
QY 480 ValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyLysArg 499
Db 1183 GTCTATGACAGTTTACCTTATCCCCAAGAGTGTGTGCTGGGGACCTTCGTGGGGGCGAGA 1242
QY 500 AspSerCysGlnGlyAspSerGlyGlyProLeuValCysGluGlnAsnAsnArgTrpTyr 519
Db 1243 GACTCTCTCCAGGAGGAGACAGCGGGGGGCTCTTGTCTGTAGAGAGACACCGCTGGTAC 1302
QY 520 LeuAlaGlyValThrSerTrpGlyThrGlyCysGlnArgAnLysProGlyValTyr 539
Db 1303 CTGGCAGGTGTACAGCTGGGGCAGAGCTGTGGCCAGAGAAACAAACCTTGTGTGTAC 1362
QY 540 ThrIysValThrGluValLeuProTyrPileTyrSerLysMetGluSerGluValArgPhe 559
Db 1363 ACCAAGTGTACAGAAAGTTCTTCCCTGGATTTCAGCAGATGAGAGCGAGGTGCGATTTC 1422
QY 560 ArgLysSer 562
|
```

1423 AGAAATCC 1431

GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Virca, G. Duke
; TITLE OF INVENTION: DENDRITIC CELL TRANSMEMBRANE SERINE PROTEASE
; FILE REFERENCE: 3256-A
; CURRENT APPLICATION NUMBER: US/10/177,661
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/299,606
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION:
US-10-177-661-3

Alignment Scores:
Pred. No.: 3,53e-147 Length: 1341
Score: 2108.00 Matches: 393
Percent Similarity: 89.62% Conservative: 4
Best Local Similarity: 88.71% Mismatches: 12
Query Match: 70.29% Indels: 34
DB: 15 Gaps: 2

US-09-879-792-12 (1-562) x US-10-177-661-3 (1-1341)

QY 120 ThrProValGlyAlaValProIleArgSerProAlaArgSerAlaProAlaThrArg 139
DB 112 TCCCCCACCCTCCATCGTCGCGACTCCTCTCCAGCCCTCATATTCCTCCCTGCCGCC 171
QY 140 AlaThrArgGluSerProGlyThrSerLeuProLysPheThrTrpArgGluGlnLys 159
DB 172 CTGCTCCTA-----GATACGAGCTGCCAAGTTCACTGGCGGGAGGCCAGAG 222
QY 160 GlnLeuProLeuIleGlyCysValLeuLeuLeuLeuLeuValSerLeuIleLe 179
DB 223 .CAGCTACCGCTCATCGGGTGCCTGCTCTCTCTCATTTGCCCTGGTGGTTCGCTCATCATC 282
QY 180 LeuPheGlnPheTrpGlnGlyHisThrGlyLeuArgTrpLysGluGlnArgGluSerCys 199
DB 283 CTCCTCCAGTTCTGGCAGGGCCACACAGGATCAGGTACAGGATCAGGAGGAGGAGCTGT 342
QY 200 ProLysHisAlaValArgCysAspGlyValValAspCysLysLeuLysSerAspGluLeu 219
DB 343 CCCAAGCAGCTGTTCGCTGTGACGGGGTGGTGGACTGCAAGCTGAAGAGTGACGAGCTG 402
QY 220 GlyCysValArgPheAspTrpAspLysSerLeuLeuLysIleTrpSerGlySerSerHis 239
DB 403 GGCCTCGGTGAGTTTGACTGGGACCAAGTCTCTGCTTAAATCTACTCTGGGTCTCCCAT 462
QY 240 GlnTrpLeuProIleCysSerSerAsnTrpAsnAspSerTrpSerGluLysThrCysGln 259
DB 463 CAGTGGCTTCCCATCTGTAGCAGCACTGAGATGACTCTACTCAGAGAGACCTGCCAG 522
QY 260 GlnLeuGlyPheGluSerAlaHisArgThrThrGluValAlaHisArgAspPheAlaAsn 279
DB 523 CAGCTGGGTTCGAG----- 537
QY 280 SerPheSerIleLeuArgTrpAsnSerThrIleGlnGluSerLeuHisArgSerGluCys 299
DB 538 -----AGGCTCGAATGC 549
QY 300 ProSerGlnArgTrpIleSerLeuGlnCysSerHisCysGlyLeuArgAlaMetThrGly 319
DB 550 CTTTCCAGCGTATATCTCTCCCTCCAGTCTCCACTCGGAGCTGAGGCCCATGACCGGG 609
QY 320 ArgIleValGlyGlyAlaLeuAlaSerAspSerLysTrpProTrpGlnValSerLeuHis 339

DB 610 CGGATCTGGAGGGGGCGCTGGCTCGGATAGCAAGTGGCTTGGCAAGTGAGTCTGCAC 669
QY 340 PheGlyThrThrHisIleCysGlyGlyThrLeuIleAlaGlnTrpValLeuThrAla 359
DB 670 TTGGCACCACCCACATCTGTGGAGGCAAGCTCATTTGACGCCCGCTGCTCATCTGCC 729
QY 360 AlaHisCysPhePheValThrArgGluValValLeuGluGlyTrpLysValTrpAlaGly 379
DB 730 GCCCAGCTGCTCTTCTGGTACCCCGGAGAGGTCTCTGGAGGGCTGGAGGTGTACCGGGC 789
QY 380 ThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGluIleIleAlaSer 399
DB 790 ACCAGCAACCTGCACCAAGTTGCTTGGAGCGCTCCATTTCCGAGATCATCATCAACAGC 849
QY 400 AsnTrpThrAspGluGluAspAspTrpAspIleAlaLeuMetArgLeuSerLysProLeu 419
DB 850 AATTACACCGATGAGGAGGAGCACTATGACATCGCCCTCATCGCGCTGTCCAAGSCCTG 909
QY 420 ThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPheSerLeu 439
DB 910 ACCCTGTCGGCTCACATCCACCTGCTTCCCTCCCATGATGACAGACCTTTAGCTTC 969
QY 440 AsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThrAspAspLysThrSer 459
DB 970 AATGAGACCTCTGGATCACAGGCTTTGGCAAGACCAGGAGACAGATGACAAGACATCC 1029
QY 460 ProPheLeuArgGluValGlnValAsnLeuIleAspPheLysCysAsnAspTrpLeu 479
DB 1030 CCTTCTCTCCGGAGGTGAGTCAATCTCATCGACTTCAAGAAATGCAATGACTACTTG 1089
QY 480 ValTrpAspSerTrpLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyArg 499
DB 1090 GTCTATGACATGTACCTTTACCCCAAGGATGATGTCTGGGAGACTTCTGGGGGGCAGA 1149
QY 500 AspSerCysGlnGlyAspSerGlyValProLeuValCysGluGlnAsnAsnArgTrpTrp 519
DB 1150 GACTCTCCAGGAGGACAGCGGGGGGCTCTTGTCTGTGAGCAGACACACCGCTGGTAC 1209
QY 520 LeuAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArgAsnLysProGlyValTrp 539
DB 1210 CTGGCAGGTGTCCACAGCTGGGGCAGAGCTGTGGCCAGAGAAACAAACCTGTGTGTAC 1269
QY 540 ThrLysValThrGluValLeuProTrpIleTrpSerLysMetGluSerGluValArgPhe 559
DB 1270 ACCAAGTGACAGAGATTTCTTCCCTGGATTTACAGCAAGATGAGGAGCGAGTGCGATT 1329
QY 560 ArgLysSer 562
DB 1330 AGAAATCC 1338

RESULT 8

US-09-898-837A-16/c
; Sequence 16, Application US/09898837A
; Publication No. US20030077697A1
; GENERAL INFORMATION:
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Herrmann, John L.
; APPLICANT: Burgess, Catherine
; APPLICANT: Fernandes, Elma
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Rastelli, Luca
; APPLICANT: Curagen Corporation
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: MacDougall, John R.
; TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: 15966-598 CIP
; CURRENT APPLICATION NUMBER: US/09/898,837A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986

US-09-879-792-12 (1-562) x US-09-879-792-35 (1-1230)

QY 180 LeuPheGlnPheTrpGlnGlyHisThrGlyIleArgTyrLysGluGlnArgGluSerCys 199
Db 28 CTAAGTCAGTTCTGGCGAGNNCCACACAGNNATCAGGTACAGAGCAGAGGAGAGCTGT 87
QY 200 ProLysHisAlaValArgCysAspGlyValValAspCysLysLeuLysSerAspGluLeu 219
Db 88 CCCAAGCAGCTGTTCCGCTGTGACGGGGTGGTGGACTGCAAGCTGAAGAGTACGAGCTG 147
QY 220 GlyCysValArgPheAspTrpAspLysSerLeuLeuLysIleTyrSerGlySerSerHis 239
Db 148 GGCCTGCGTAGGTTGACTGGGACAGTCTCTGCTTTAAATCTACTCTGGGCTCCCTCCAT 207
QY 240 GlnTrpLeuProLysCysSerSerAsnTrpAsnAspSerTyrSerGluLysThrCysGln 259
Db 208 CAGTGGCTTCCCATCTGTAGAGCAACTGGAATGACTCTCTACTCAGAGAAGACTGCCAG 267
QY 260 GlnLeuGlyPheGluSerAlaHisArgThrThrGluValAlaHisArgAspPheAlaAsn 279
Db 268 CAGCTGGGTTTCCAGAGTCTCCACGGACACCGAGTTGCCACAGGGATTGTCACAC 327
QY 280 SerPheSerIleLeuArgTyrAsnSerThrIleGlnGluSerLeuHisArgSerGluCys 299
Db 328 AGCTTCTCAATCTTGAGATACAACTCCACCATCCAGAAAGCTCCACAGGCTCTGAATGC 387
QY 300 ProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeuArgAlaMetThrGly 319
Db 388 CCTTCCAGCGGTATATCTCTCCAGTGTTCCTCAGTCTGGACTGAGGGCCATGACCGGG 447
QY 320 ArgIleValGlyGlyAlaLeuAlaSerAspSerLysTyrProTrpGlnValSerLeuHis 339
Db 448 CGGATCGTGGAGGGCGCGTCCGCTCGGATAGCAAGTGGCCCTTGGCAAGTGTACCGGGC 507
QY 340 PheGlyThrThrHisIleCysGlyGlyThrIleAspAlaGlnTrpValLeuThrAla 359
Db 508 TTCGGACCAACCACATCTGTGGAGCAGCTCATTTGACGCCAGTGGGTGTCTCATCGCC 567
QY 360 AlaHisCysPhePheValThrArgGluLysValLeuGluGlyTrpLysValTrpAlaGly 379
Db 568 GCCCACTGCTTCTGTGACCGCGGAGAGGTCCTGGAGGCTGGAGGTGTACCGGGC 627
QY 380 ThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGluIleIleAsnSer 399
Db 628 ACCAGCAACCTGCACAGTTGCTGAGGAGCTCCATTTGCCAGATCATCATCAACAGC 687
QY 400 AsnTyrThrAspGluAspAspTyrAspIleAlaLeuMetArgLeuSerLysProLeu 419
Db 688 AATTACCGATGAGAGAGCACTATGACATCGCCCTCATCGGGCTGTCCAAGCCCTGT 747
QY 420 ThrLeuSerAlaHis-----IleHisProAlaCysLeuProMetHisGly 434
Db 748 ACCCTGTCCGGTGGAGGAATCTGCACTCCCGCTCTCTGCTGCCCGCCAGCCAGCCCT 807
QY 435 ---GlnThrPheSerLeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGlu 453
Db 808 CTGCGCCCTCGCATCTGTGCAGCATCT-----GTCAACTCATATCCGGGCCCCCAAGCT 861
QY 454 ThrAspAspLysThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLys 473
Db 862 TCTGCAGACAGACATCCCTTCTCTCGGAGGTCGAGGTCAATCTCATCGACTTCAAG 921
QY 474 LysCysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGly 493
Db 922 AAATGCAATGACTACTTGTCTATGACAGTTACCTTACCCCAAGGATGATGTGCTCGG 981
QY 494 AspLeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGlu 513
Db 982 GACCTTCGTGGGGCAGAGACTCCCTGCGAGGAGAGCAGCGGGGGCCCTCTTGTCTGTGAG 1041
QY 514 GlnAsnAsnArgTyrTyrLeuAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArg 533

Db 1042 CAGAAACAACCGCTGGTACTGTCAGAGTGTTCACAGCTGGGGCAGCAGGCTGTGGCCAGAGA 1101
QY 534 AsnLysProGlyValTyrThrLysValThrGluValLeuProTrpIleTyrSerLysMet 553
Db 1102 AACAAACCTGGTGTGTACACCAAGTGCAGAAAGTTCTTCCCTGGATTTACAGCAAGATG 1161
QY 554 GluSerGluValArgPheArgLysSer 562
Db 1162 GAGGC-GAGGTGCGATTTCAGAAAATCC 1187

RESULT 10

US-09-804-156-5
; Sequence 5, Application US/09804156
; Patent No. US20020068320A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Serine protease Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT005P4
; CURRENT APPLICATION NUMBER: US/09/804,156
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/189,025
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-804-156-5

Alignment Scores:

Pred. No.: 1.75e-97 Length: 1222
Score: 1436.00 Matches: 260
Percent Similarity: 99.24% Conservative: 2
Best Local Similarity: 98.48% Mismatches: 2
Query Match: 47.88% Indels: 0
DB: Gaps: 0

US-09-879-792-12 (1-562) x US-09-804-156-5 (1-1222)

QY 295 HisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeu 314
Db 10 CACAGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCAGTGTCCCACTCGGACTG 69
QY 315 ArgAlaMetThrGlyArgIleValGlyGlyAlaLeuAlaSerAspSerLysTrpProTrp 334
Db 70 AGGGCATGACCGGCGGATGTGGAGGGGCGCTGGCTCGATAGCAAGTGGCTTGG 129
QY 335 GlnValSerLeuHisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGln 354
Db 130 CAAGTGAGTCTGCACTTCGGCACCACCCACATCTGTGGAGGCACTCATTCAGCCCCAG 189
QY 355 TrpValLeuThrAlaAlaHisCysPhePheValThrArgGluLysValLeuGluGlyTrp 374
Db 190 TGGGTGCTCATCTGCGGCCACTGCTTCTTCTGTGACCCCGGAGAGGTCTCTGAGGGCTGG 249
QY 375 LysValTyrAlaGlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGlu 394
Db 250 AAGGTGACGCGGCGGACCGGACCACTGACCACTGCTGAGCGAGCTTCATTGCCGAG 309
QY 395 IleIleIleAsnSerAsnTyrThrAspGluAspAspTyrAspIleAlaLeuMetArg 414
Db 310 ATCATCATCAACAGCAATTACACCGATGAGGAGGACGACTATGACATCGCCCTCATGCGG 369
QY 415 LeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGly 434
Db 370 CTGTCCAAAGCCCTTGACCCCTGTCCGCTCACAATCCACCTGTCTGCTCCCATGTCATGGA 429
QY 435 GlnThrPheSerLeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThr 454
Db 430 CAGACCTTACCTCATGAGACCTGCTGGATCACAGGCTTTGGCAGAGCAGGAGACA 489
QY 455 AspAspLysThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLys 474


```

Db      490  GATGCAAGACATCCCTTCTCCGGAGGTGCAGGTCAATCTCATCGACTTCAAGAAA 549
QY      475  CysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAsp 494
Db      550  TGCATATGACTACTTGTCTATCAGACAGTACCTTACCCCAAGCATGATGTCTGGGAC 609
QY      495  LeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyProLeuValCysGluGln 514
Db      610  CTTCTGTGGGGGAGAGACTCTCTGCCAGGGAGAGACAGCGGGGGGCTCTCTGTCTGTGAGCAG 669
QY      515  AsnAsnArgTyrTyrLeuAlaGlyValThrSerTyrGlyThrGlyCysGlyGlnArgAsn 534
Db      670  AACACCGCTGTGTACTCTGCAGGTGTCCAGCTGGGGGCACAGGCTGTGGCCAGAGAAAC 729
QY      535  LysProGlyValTyrThrLysValThrGluValLeuProTyrPileTyrSerLysMetGlu 554
Db      730  AAACCTGGTGTGTACACCAAGTGCAGAGTCTTCTCCCTGGATTTACAGCAAGATGGAG 789
QY      555  SerGluValArg 558
Db      790  AACAGAGCTCAG 801

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RESULT 11

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US-09-946-633-3
; Sequence 3, Application US/09946633
; Patent No. US20020119925A1
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: PT005P1
; FILE REFERENCE: Serine proteases
; CURRENT APPLICATION NUMBER: US/09/946,633
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 60/133,239
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/135,163
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/147,005
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/152,935
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/162,979
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-633-3

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Alignment Scores:

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Pred. No.: 1,75e-97 Length: 1222
Score: 1436.00 Matches: 260
Percent Similarity: 99.24% Conservative: 2
Best Local Similarity: 98.48% Mismatches: 2
Query Match: 47.88% Indels: 0
DB: 10 Gaps: 0

```

US-09-879-792-12 (1-562) x US-09-946-633-3 (1-1222)

```

QY      295  HisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeu 314
Db      10  CACAGGTCTGAATGCCCTTCCAGCGGTATATCTCCCTCCAGTGTTCCTCCAGTGGAGCTG 69
QY      315  ArgAlaMetThrGlyArgIleValGlyGlyAlaLeuAlaSerAspSerLysTyrProTyr 334
Db      70  AGGGCCATGACCGGGCGGATCGTGGAGGGGCGCTGGGCTCGGATAGCAAGTGGCTTGG 129
QY      335  GlnValSerLeuHisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGln 354

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Db      130  CAAAGTGAGTCTGCATCTTCGGGCACCCACCATCTCTGTGGAGGCACCGCTCATTTGACGCCAG 189
QY      355  TrpValLeuThrAlaAlaHisCysPhePheValThrArgGluLysValLeuGluGlyTyr 374
Db      190  TGGGTGCTCAGTCCGCCCCACATCTCTTCTGTGTGACCCGGGAGAGAGGTCTCTGGAGGGCTGG 249
QY      375  LysValTyrAlaGlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGlu 394
Db      250  AAGGTGTATACCGGGGACACCAAGCACTGTGCACACAGTGTCTGTGAGCGAGCTCCATTGCCGAG 309
QY      395  IleIleIleAsnSerAsnTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArg 414
Db      310  ATCATCATCAACAGCAATTTACACCGATGAGGAGGACGACTATGACATCCGCCCTCATGCCG 369
QY      415  LeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGly 434
Db      370  CTGTCCAGGCCCTGTGACCTGTCCGCTCACATCCACCTGCTTGTCTCCCATGCAATGGA 429
QY      435  GlnThrPheSerLeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThr 454
Db      430  CAGACCTTTAGCCTCAATGAGACCTGTCTGGATCACAGGCTTTGGCAAGACCCAGGGAGACA 489
QY      455  AspAspLysThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLys 474
Db      490  GATGCAAGACATCCCTTCTCCGGAGGTGCAGGTCAATCTCATCTCATCAAGAAA 549
QY      475  CysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAsp 494
Db      550  TGCATATGACTACTTGTCTATGACAGTGTACCTTACCCCAAGCATGATGTCTGGGAC 609
QY      495  LeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyProLeuValCysGluGln 514
Db      610  CTTCTGTGGGGGAGAGACTCTCTGCCAGGGAGAGACAGCGGGGGGCTCTCTGTGTGAGCAG 669
QY      515  AsnAsnArgTyrTyrLeuAlaGlyValThrSerTyrGlyThrGlyCysGlyGlnArgAsn 534
Db      670  AACACCGCTGTGTACTCTGCAGGTGTCCAGCTGGGGGCACAGGCTGTGGCCAGAGAAAC 729
QY      535  LysProGlyValTyrThrLysValThrGluValLeuProTyrPileTyrSerLysMetGlu 554
Db      730  AAACCTGGTGTGTACACCAAGTGCAGAGTCTTCTCCCTGGATTTACAGCAAGATGGAG 789
QY      555  SerGluValArg 558
Db      790  AACAGAGCTCAG 801

```

RESULT 12

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US-10-319-519-5
; Sequence 5, Application US/10319519
; Publication No. US20030175938A1
; GENERAL INFORMATION:
; APPLICANT: Shi et al.
; TITLE OF INVENTION: Serine Protease Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT005P5
; CURRENT APPLICATION NUMBER: US/10/319,519
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 10/125,459
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 09/597,842
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 09/597,843
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 10/067,761
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 09/946,633
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US 09/804,156
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/US00/12207
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/189,025

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; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/162,979
; PRIOR FILING DATE: 1999-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-319-519-5

Alignment Scores:
Pred. No.: 1,75e-97 Length: 1222
Score: 1436.00 Matches: 260
Percent Similarity: 99.24% Conservative: 2
Best Local Similarity: 98.48% Mismatches: 2
Query Match: 47.88% Indels: 0
DB: 13 Gaps: 0

US-09-879-792-12 (1-562) x US-10-319-519-5 (1-1222)
QY 295 HisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeu 314
DB 10 CACAGGTCTGATGCGCTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACTG 69
QY 315 ArgAlaMetThrGlyArgIleValGlyAlaLeuAlaSerAspSerLysTrpProTrp 334
DB 70 AGGGCCATGACCGGGCGGATCGTGGAGGGGGCTGGCTCGGATAGCAAGTGGGCTTGG 129
QY 335 GlnValSerLeuHisPheGlyThrHisIleCysGlyGlyThrIleLeuLeuAspAlaGln 354
DB 130 CAAGTGAGTCTGACTTGGCACCACCCACATCTGTGGAGGCGCGCTCATTCAGCCCCAG 189
QY 355 TrpValLeuThrAlaAlaHisCysPheValThrArgGluLysValLeuGluGlyTrp 374
DB 190 TGGGTGCTCAGTCCGCCCTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACTG 249
QY 375 LysValTyrAlaGlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGlu 394
DB 250 AAGGTGTACGGGGCAGCACCAACCTGCACCAAGTGTGCTGAGGCGAGCTCCATTCGCGAG 309
QY 395 IleIleIleAsnSerAsnTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArg 414
DB 310 ATCATCATCAACAGCAATTTACCCGATGAGGAGGAGACTATGATCGCCCTCCATGCGA 369
QY 415 LeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGly 434
DB 370 CTGTCCAAAGCCCTGACCTGTCGCTCACATCCACCTGCTTGCCTCCCATGCAATGGA 429
QY 435 GlnThrPheSerLeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThr 454
DB 430 CAGACCTTTAGCTCAATGAGACCTGCTGATCACAGGCTTTGGCAAGACCCAGGAGACA 489
QY 455 AspAspLysThrSerProPheLeuArgGluValGlnValAsnLeuLeuAspPheLysLys 474
DB 490 GATGACACAGCAATTCCTCTCCGGAGGTGCAGGTCAATCTCATGCACTTCAAGAAA 549
QY 475 CysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAsp 494
DB 550 TGCATATGACTACTTGTGCTATGACAGTTACCTTACCCCAAGGATGATGTGCTGGGAC 609
QY 495 LeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyProLeuValCysGluGln 514
DB 610 CTTCTGGGGGGCAGAGACTCTCCGACGGGAGAGCAGCGGGGGGCTCTGTGCTGTGAGCAG 669
QY 515 AsnAsnArgTyrTyrLeuAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArgAsn 534
DB 670 AACACCGCTGTGTACTGTCAGAGGTGTACCACTGGGGCAGAGGCTGTGGCCAGAGAAC 729
QY 535 LysProGlyValTyrThrLysValThrGluValLeuProTrpIleTyrSerLysMetGlu 554
DB 730 AAACCTGGTGTGTACACCAAGTGTACAGAGTTCTTCCCTCGATTTTACAGCAAGATGGAG 789
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QY 555 SerGluValArg 558
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; Sequence 3, Application US/10125459
; Publication NO. US20020192800A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: PT005P1
; FILE REFERENCE: Serine proteases
; CURRENT APPLICATION NUMBER: US/10/125,459
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/597,839
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 60/133,239
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/135,163
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 60/147,005
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/152,935
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/162,979
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1222
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-125-459-3

Alignment Scores:
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Score: 1436.00 Matches: 260
Percent Similarity: 99.24% Conservative: 2
Best Local Similarity: 98.48% Mismatches: 2
Query Match: 47.88% Indels: 0
DB: 14 Gaps: 0

US-09-879-792-12 (1-562) x US-10-125-459-3 (1-1222)
QY 295 HisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeu 314
DB 10 CACAGGTCTGATGCGCTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACTG 69
QY 315 ArgAlaMetThrGlyArgIleValGlyAlaLeuAlaSerAspSerLysTrpProTrp 334
DB 70 AGGGCCATGACCGGGCGGATCGTGGAGGGGGCTGGCTCGGATAGCAAGTGGGCTTGG 129
QY 335 GlnValSerLeuHisPheGlyThrHisIleCysGlyGlyThrIleLeuLeuAspAlaGln 354
DB 130 CAAGTGAGTCTGACTTGGCACCACCCACATCTGTGGAGGCGCGCTCATTCAGCCCCAG 189
QY 355 TrpValLeuThrAlaAlaHisCysPheValThrArgGluLysValLeuGluGlyTrp 374
DB 190 TGGGTGCTCAGTCCGCCCTCCAGCGGTATATCTCCCTCCAGTGTCCCACTGGGACTG 249
QY 375 LysValTyrAlaGlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGlu 394
DB 250 AAGGTGTACGGGGCAGCACCAACCTGCACCAAGTGTGCTGAGGCGAGCTCCATTCGCGAG 309
QY 395 IleIleIleAsnSerAsnTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArg 414
DB 310 ATCATCATCAACAGCAATTTACCCGATGAGGAGGAGACTATGATCGCCCTCCATGCGA 369
QY 415 LeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGly 434
DB 370 CTGTCCAAAGCCCTGACCTGTCGCTCACATCCACCTGCTTGCCTCCCATGCAATGGA 429
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Score: 1282.50 Matches: 266
Percent Similarity: 95.39% Conservative: 3
Best Local Similarity: 94.33% Mismatches: 10
Query Match: 42.76% Indels: 9
DB: 9 Gaps: 0

US-09-879-792-12 (1-562) x US-09-879-792-28 (1-834)

QY 219 LeuGlyCysValArgPheAspTyrAspLysSerLeuLeuLysIleTyrSerGlySerSer 238
Db 2 CTGGGCTGGCTGAGGTTTGGTGGACAAAGTCTCTGCTTAAATCTACTCTGGGTCTCC 61

QY 239 HisGlnTyrLeuProIleCysSerSerAsnTyrAsnAspSerTyrSerGlyLysThrCys 258
Db 62 CATCAGTGGCTTCCCATCTGTAGCAGCAACTGGAAATGACTCTCTACTCTCAGAGAAGACCTGC 121

QY 259 GlnGlnLeuGlyPheGluSerAlaHisArgThrThrGluValAlaHisArgAspPheAla 278
Db 122 CAGCAGCTGGGTTTGGAGGTGCTCACCGGACAAACGAGGTTGCCACAGGGATTTTGCC 181

QY 279 AsnSerPheSerIleLeuArgTyrAsnSerThrIleGlnGluSerIleHisArgSerGlu 298
Db 182 AACAGCTTCTCAATCTGAGATACAACTCCACCATCCAGAAAGCTCCACAGGCTCGAA 241

QY 299 CysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeuArgAlaMetThr 318
Db 242 TGCCCTTCCACGGGTATATCTCCCTCCAGTGTCCCACTGCGGACTGAGGGCCATGACC 301

QY 319 GlyArgIleValGlyAlaLeuAlaSerAspSerLysTyrProTyrGlnValSerLeu 338
Db 302 GGGCGGATCGTGGAGGGGCGTGGCTCGGATAGCAAGTGGCTTGGCAAGTGGTCTG 361

QY 339 HisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGlnTyrValLeuThr 358
Db 362 CACTTCGGCACCACCATCTGTGGAGGACGCTCATTTGACGCCCGCCAGTGGGTGCTCACT 421

QY 359 AlaAlaHisCysPhePheValThrArgGluLysValLeuGluGlyTyrLysValTyrAla 378
Db 422 GCCGCCCATCTGCTTCTGTAACCCGGAGAGGTCCTGGAGGGCTGGAGGTGTACGGC 481

QY 379 GlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGluIleIleLeuAsn 398
Db 482 GGCACCAGCAACTG-CACCAGTTGCTTGAGGCAGC-TCCATTGCCGAGATCATCATCAAC 539

QY 399 SerAsnTyrThrAspGluGluAspAspTyr-AspIleAlaLeuMetArgLeu-SerLysP 418
Db 540 AGCAATTACACCGATGAGGAGGACGACTATTGACATCGCCCTCATGCGGCTGTCCAAGC 599

QY 418 roLeuThrLeuSerAlaHisIleHisProAlaCysLeu-ProMetHisGlyGlnThrPhe 437
Db 600 CCTGAACCTGTCCGT-CACATCCACCCCTGCTTGCTCCCCCATGATGACAGACCTTT 658

QY 438 SerLeuAsnGluThrCysTyrIleThrGlyPheGlyLysThrArgGluThrAspAspLys 457
Db 659 AGCCTCAATGAGACCTGTGGATCACAGGCTTTGGCAAGACAGAGGAGACAGATCAAAAG 718

QY 458 ThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysCysAsnAsp 477
Db 719 ACATCCCCCTTCCCT-CGGAGGTGAGGTCATCTCATCGACTTCCAGAAATGCAATGAC 777

QY 478 TyrLeuValTyrAspSerTyrTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGly 497
Db 778 TAACTGGTCTATGACAGTACCTTAC--CCAGGATGATGTGTGT-GGGGAACCTCTGTGG 834

Search completed: December 17, 2003, 22:09:17
Job time : 484 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 17, 2003, 20:10:37 ; Search time 104 Seconds

(without alignments)
2385.167 Million cell updates/sec

Title: US-09-879-792-12

Perfect score: 2999

Sequence: 1 MERDSHGNSPARTPSAGAS.....TEVLPWYKMESEVRFKKS 562

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: /cgm2_6/ptodata/2/ina/5B_COMB.seq:
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6: /cgm2_6/ptodata/2/ina/backfiles.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	740.5	24.7	1479	4	US-09-691-840-1
3	736.5	24.6	2479	3	US-09-342-749-29
4	736.5	24.6	2479	4	US-09-691-840-29
5	727.5	24.3	2413	3	US-09-518-046-1
6	713	23.8	2079	4	US-09-656-002-1
7	708	23.6	2544	3	US-09-518-046-3
8	707.5	23.6	2038	3	US-09-008-271A-18
9	694.5	23.2	2416	3	US-09-261-416-1
10	666	22.2	2363	4	US-09-742-703-3
11	642.5	21.4	1783	3	US-09-510-738A-188
12	642.5	21.4	1783	4	US-09-861-966-188

13	622.5	20.8	610	4	US-09-280-116-22	Sequence 22, Appl
14	619.5	20.7	1605	2	US-09-000-846-1	Sequence 1, Appl
15	612	20.4	1615	4	US-09-820-002-1	Sequence 1, Appl
16	594.5	19.8	1077	3	US-08-807-151-2	Sequence 2, Appl
17	594.5	19.8	1077	4	US-09-478-957-2	Sequence 2, Appl
18	584.5	19.5	3147	2	US-09-027-337-1	Sequence 1, Appl
19	584.5	19.5	3147	4	US-09-644-600-1	Sequence 1, Appl
20	584.5	19.5	3147	4	US-09-644-600-18	Sequence 18, Appl
21	548.5	18.3	2581	5	PCT-US94-00616-1	Sequence 1, Appl
22	548.5	18.3	2581	5	PCT-US94-00616-1	Sequence 1, Appl
23	524.5	17.5	2900	2	US-09-027-337-9	Sequence 9, Appl
24	524.5	17.5	2900	4	US-09-644-600-9	Sequence 9, Appl
25	520	17.3	1724	6	5200340-5	Patent No. 5200340
26	513.5	17.1	1081	3	US-09-008-271A-15	Sequence 15, Appl
27	512	17.1	1103	2	US-09-016-366A-24	Sequence 24, Appl
28	510.5	17.0	1094	4	US-09-023-942A-3	Sequence 3, Appl
29	508.5	17.0	1100	4	US-09-023-942A-5	Sequence 5, Appl
30	508	16.9	1097	2	US-08-978-404B-4	Sequence 4, Appl
31	505	16.8	1108	2	US-09-016-366A-14	Sequence 14, Appl
32	505	16.8	1108	2	US-08-978-404B-20	Sequence 20, Appl
33	502	16.7	1739	2	US-08-681-151-2	Sequence 2, Appl
34	501	16.7	959	4	US-09-023-942A-25	Sequence 25, Appl
35	500	16.7	1142	4	US-09-386-642-8	Sequence 8, Appl
36	500	16.7	1169	4	US-09-386-642-7	Sequence 7, Appl
37	493.5	16.5	2296	1	US-07-750-080A-18	Sequence 18, Appl
38	493.5	16.5	2296	3	US-08-651-472-18	Sequence 18, Appl
39	493.5	16.5	2296	3	US-08-358-928-18	Sequence 18, Appl
40	493.5	16.5	2430	4	US-09-192-012-4	Sequence 4, Appl
41	493.5	16.5	2679	6	5200340-7	Patent No. 5200340
42	493.5	16.5	2753	1	US-07-854-603-1	Sequence 1, Appl
43	492.5	16.4	2497	1	US-08-643-219-12	Sequence 12, Appl
44	492.5	16.4	2497	2	US-09-131-995-12	Sequence 12, Appl
45	492.5	16.4	2497	2	US-08-832-087B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-342-749-1
; Sequence 1, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TWERS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 60/091,044
; EARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1476)
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (724)
; OTHER INFORMATION: Listed as T in GenBank Accession No. U75329
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (985)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
; FEATURE:
; NAME/KEY: conflict
; LOCATION: (1347)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329

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FEATURE:
NAME/KEY: conflict
LOCATION: (1466)
OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329
FEATURE:
NAME/KEY: conflict
LOCATION: (1471)
OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329.
FEATURE:
NAME/KEY: allele
LOCATION: (478)
OTHER INFORMATION: This base can be G or A with G being the more
OTHER INFORMATION: common allele. The codon will change from Val to
OTHER INFORMATION: Met.
FEATURE:
NAME/KEY: allele
LOCATION: (777)
OTHER INFORMATION: This base can be C or T with C being the more
OTHER INFORMATION: common allele. The codon is unaffected with both
OTHER INFORMATION: alleles encoding Gly.
FEATURE:
NAME/KEY: allele
LOCATION: (768)
OTHER INFORMATION: This base can be C or T with C being the more
OTHER INFORMATION: common allele. This is a silent polymorphism.
FEATURE:
NAME/KEY: allele
LOCATION: (834)
OTHER INFORMATION: This base can be C or T with C being the more
OTHER INFORMATION: common allele. This is a silent polymorphism.
FEATURE:
NAME/KEY: allele
LOCATION: (625)
OTHER INFORMATION: This base can be T or A with T being the more
OTHER INFORMATION: common allele. The codon will change from Phe to
OTHER INFORMATION: Ile
US-09-342-749-1

Alignment Scores:
Pred. No.: 2,716-30 Length: 1479
Score: 740.50 Matches: 178
Percent Similarity: 47.49% Conservative: 87
Best Local Similarity: 31.90% Mismatches: 194
Query Match: 24.69% Indels: 99
DB: 3 Gaps: 18
US-09-879-792-12 (1-562) x US-09-342-749-1 (1-1479)

QY 27 AlaGlyThrProGlyArgAla-----SerProAlaGln 38
DB 13 TCAGGTCACCCAGCCTATTGGACCTTACTATGAAACCATGGATACCAACCGGAAAC 72
QY 39 AlaSerProAlaGlnAlaSerProAlaGlyThrProGlyArgAlaSerProAlaGln 58
DB 73 CCCTATCCGCACAGCCCACTGTGTCCTCCACT---GTCTACGAGTGTGATCGGCTCAG 129
QY 59 AlaSerProAlaGlyThrProGlyArgAlaSerProGlyArgAlaSerProAlaGln 78
DB 130 TACTACCGCTCCCGCTGCC-----CAGTACGCGCCGAGGGTC 168
QY 79 AlaSerProAlaArgAlaSerProAlaLeuAlaSerLeuSerArgSerSerGlyArg 98
DB 169 CTGACGCGGCT---TCCAACCCCGCTGCTGTCAGCAGCCCAATCCCATCCCGG--- 222
QY 99 SerSerAlaArgSerAlaSerValThrThrSerProThrArgValThrLeuValArg 118
DB 223 -----ACAGTGTGCACCTCAAGACTAAGAACTGTGTCATC 261
QY 119 AlaThrProValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaThr 138
DB 262 ACCTTGACCTGGGACCTTC----- 282
QY 139 ArgAlaThrArgGluSerProGlyThrSerLeuProLysPheThrTyrArgGluGlyGln 158

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Db 282 ----- 282
QY 159 LysGlnLeuProLeuIleGlyCysValLeuLeuLeuLeuLeuValValSerLeuLeu 178
Db 283 -----CTCGTGGAGCT-----GCGTGGCGCTGCGCTACTC 315
QY 179 IleLeuPheGlnPheTyrGln-----GlyHisThrGlyLeuArgTyr 192
Db 316 -----TGGAGTTCATGGGAGCGACAGTGTCTCCAACTCTGGGATAGAGTGC 360
QY 193 LysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValAlaAspCys 212
Db 361 ---GACTCTCTCAGGTACCTGCATCAACCCCTCTAAGTGTGTGATGGGTGCACACTGC 417
QY 213 LysLeuLysSerAspGluLeuGlyCysValArgPheAspTyrPaspLysSerLeuLeuLys 232
Db 418 CCGCGCGGAGGAGCAGAGATCGGTGTGTTTCGCTCTACGGACCAAACTTCATCTTCAG 477
QY 233 IleTyrSerGlySerSerHisGlnTyrLeuProIleCysSerSerAsnTyrAsnAspSer 252
Db 478 GTGTACTCATCTCAGAGGAGTCTGCGACCTGTGTGCCAAGACGACTGGACGAGAAC 537
QY 253 TyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrGluVal 272
Db 538 TACGGCGCGGCGCTGCAGGACATGGGCTATAGATAATATTTTACTCTAGCCAA--- 594
QY 273 AlaHisArgAspPheAlaAsnSerPheSerIleLeuArgTyrAsnSerThr----- 289
Db 595 GGAATAGTGGATGACAGCGGATCCACAGCTTTATGAAACTGAACACAAAGTGGCGCAAT 654
QY 290 -----IleGlnGluSerLeuHisArgSerGlu---CysProSerGlnArgTyrIleSer 306
Db 655 GTGCGATATCTATGAAACTGTACCAAGTGTGCTGTCTTCAAAGCAGTGGTTCT 714
QY 307 LeuGlnCysSerHisCysGlyLeuArg-----AlaMetThrGlyArgIleValGly 323
Db 715 TTACGCTGTATAGCTCGCGGCTCAACTTGAACCTCAAGCGCGCAGAGCAGGATCGTGGGC 774
QY 324 GlyAlaLeuAlaSerAspSerLysTyrProTyrGlnValSerLeuHisPheGlyThrThr 343
Db 775 GCGCAGAGCGCGCTCCCGGGGCGCTCGGCTCGCAGCTGAGCTGCAGCTCCAGAACGTC 834
QY 344 HisIleCysGlyGlyThrLeuIleAspAlaGlnTyrValLeuThrAlaAlaHisCysPhe 363
Db 835 CAGGTGTGCGGAGGCTCCATCATCACCCTGAGTGTGTCGACGCGCCCTCGCTCGTG 894
QY 364 PheValThrArgGluLysValLeuGluGly-----TyrLysValTyrAlaGlyThr 380
Db 895 -----GAAAAACCTCTTAACAATCCATGGCATTTGACGCGCATTTGCGGGATT 942
QY 381 SerAsnLeuHisGlnLeuProGluAlaAla-----SerIleAlaGluIleIleAsn 398
Db 943 TTGAGACAATCTTTCTGTTCTATGAGCGCGGATACCAAGTAGAAGAAAGTGTATTCAT 1002
QY 399 SerAsnTyrThrAspGluGluAspTyrAspIleAlaLeuMetArgLeuSerLysPro 418
Db 1003 CCAAAATATGACTCAAGACCAAGACCAATGACATGGCTGTGATGAGCTGCAGAGCTC 1062
QY 419 LeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPheSer 438
Db 1063 CTGACTTTCAACAGCACTAGTAGAAACCACTGTGTCTGCCCAACCCAGGCATGATGTGCAG 1122
QY 439 LeuAsnGluThrCysTyrIleThrGlyPheGlyThrArgGluThrAspAspLysThr 458
Db 1123 CCAGAACAGCTCTGCTGTGATTTCCGGGTGGGGGCCACCCAGAGAG---AAAGGGAAGACC 1179
QY 459 SerProPheLeuArgGluValGlnValAsnLeuLeuAspPheLeuLysCysAsnAspTyr 478
Db 1180 TCAGAGGTGCTGAACGCTGCCAGGTGCTTCTCATTTGAGACACAGAGATGCAACAGCAGA 1239
QY 479 LeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyGly 498

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Db 1300 GTGATTTCTTCCAGGCTGACAGTGGAGGGCTCTGTCTCACTTCCGAAGAACAAATATCTGG 1359
Qy 519 TyrLeuAlaGlyValThrSerTTPGlyThrGlyCysGlyGlnArgAsnLysProGlyVal 538
Db 1360 TGGCTGATAGGGGATCAAGCTGGGTTCTGGCTGTGCCAAAGCTTACAGACCGAGGATG 1419
Qy 539 TyrThrLysValThrGluValLeuProTTPLeuTyrSerLysMetGluSerGlu 556
Db 1420 TACGGGAATGTGATTCACGACTGGATTATCGACAAATGAGGGCAGAC 1473

RESULT 2

US-09-691-840-1
; Sequence 1, Application US/09691840
; Patent No. 644419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TWPSS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1476)
; NAME/KEY: conflict
; LOCATION: (724)
; OTHER INFORMATION: Listed as T in GenBank Accession No. U75329
; NAME/KEY: conflict
; LOCATION: (985)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 644419 U75329
; NAME/KEY: conflict
; LOCATION: (1347)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 644419 U75329
; NAME/KEY: conflict
; LOCATION: (1466)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 644419 U75329
; NAME/KEY: conflict
; LOCATION: (1471)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 644419 U75329
; NAME/KEY: allele
; LOCATION: (478)
; OTHER INFORMATION: This base can be G or A with G being the more
; OTHER INFORMATION: common allele. The codon will change from Val to
; OTHER INFORMATION: Met.
; NAME/KEY: allele
; LOCATION: (777)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. The codon is unaffected with both
; OTHER INFORMATION: alleles encoding Gly.
; NAME/KEY: allele
; LOCATION: (768)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.
; NAME/KEY: allele
; LOCATION: (834)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.

; NAME/KEY: allele
; LOCATION: (625)
; OTHER INFORMATION: This base can be T or A with T being the more
; OTHER INFORMATION: common allele. The codon will change from Phe to Ile
US-09-691-840-1
Alignment Scores:
Pred. No.: 2,71e-30 Length: 1479
Score: 740.50 Matches: 178
Percent Similarity: 47.49% Conservative: 87
Best Local Similarity: 31.90% Mismatches: 194
Query Match: 24.69% Indels: 99
DB: 4 Gaps: 18
US-09-879-792-12 (1-562) x US-09-691-840-1 (1-1479)
Qy 27 AlaGlyThrProGlyArgAla-----SerProAlaGln 38
Db 13 TCAGGGTCACCAACGACGCTATTGGACCTTACTATGAAACACCATGATACCAACCGGAAAC 72
Qy 39 AlaSerProAlaGlnAlaSerProAlaGlyThrProGlyArgAlaSerProAlaGln 58
Db 73 CCTATCCCGCACAGCCACTGTGTCCTCCACT--GTCTACGAGGTGCATCCGGCTCAG 129
Qy 59 AlaSerProAlaGlyThrProGlyArgAlaSerProGlyArgAlaSerProAlaGln 78
Db 130 TACTACCCGTCCTCCCGCTGCTCCCTC-----CAGTACGCCCCGAGGGTC 168
Qy 79 AlaSerProAlaGlyThrProAlaSerProAlaLeuAlaSerLeuSerArgSerSerGlyArg 98
Db 169 CTGACGAGGCT---TCACCCCGCTGCTGTCGACGAGCCCAATCCCATCCGG--- 222
Qy 99 SerSerSerAlaArgSerAlaSerValThrThrSerProThrArgValTyrLeuValArg 118
Db 223 -----ACAGTGTGCACCTCAAGACTAAGAAAGACCTGTGCATC 261
Qy 119 AlaThrProValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaThr 138
Db 262 ACCTTGACCTTGGGGACCTTC----- 282
Qy 139 ArgAlaThrArgGluSerProGlyThrSerLeuProLysPheThrTTPArgGluGlyGln 158
Db 282 ----- 282
Qy 159 LysGlnLeuProLeuIleGlyCysValLeuLeuLeuIleAlaLeuValValSerLeuIle 178
Db 283 -----CTGCTGGGAGCT-----GCGCTGGCGCTGGCTACTC 315
Qy 179 IleLeuPheGlnPheTTPGln-----GlyHisThrGlyIleArgTyr 192
Db 316 -----TGAAGTTTCATGGCGCAGCAAGTCTCCAACTCTGGGATAGAGTGC 360
Qy 193 LysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValValAspCys 212
Db 361 ---GACTCTCTCAGTACTGCTGATCAACCCCTCTAACTGTGTGTGATGGGTGTCACTGTC 417
Qy 213 LysLeuLysSerAspGluLeuGlyCysValArgPheAspTTPAspLysSerLeuLeuLys 232
Db 418 CCGCGCGGGGAGGAGAGATCGGTGTGTTCCTCTACGCGACCAAACTTCATCTCTCAG 477
Qy 233 IleTyrSerGlySerSerHisGlnTTPLeuProIleCysSerSerAsnTTPAsnAspSer 252
Db 478 GTGTACTCATCTCAGAGGAGTCTCTGGCACCTCTGTGTGCCAAGCACTGCAAGCAGAAC 537
Qy 253 TyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThrGluVal 272
Db 538 TACGGCGGGGGCTCGAGGACATGGCTATAGAAATATTTTACTCTAGCCAA--- 594
Qy 273 AlaHisArgAspPheAlaAsnSerPheSerIleLeuArgTyrAsnSerThr----- 289
Db 595 GGAATAGTGGATGACAGCGGATCCACGAGCTTTATGAACTGTAACACACAGTCCGCGCAAT 654
Qy 290 -----IleGlnGluSerLeuHisArgSerGlu---CysProSerGlnArgTyrIleSer 306

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Db      655  GTCCGATCTATATAAACTGACACAGTGTGCTCTTCAAAAAGCAGTGGTTCT 714
Qy      307  LeuGlnCysSerHisCysGlyLeuArg-----AlaMetThrGlyArgIleValGly 323
Db      715  TTACGCTGTATAGCTCGGGGTCACTTGAACTCAAGCCGCCAGCAGGATCGTGGGC 774
Qy      324  GlyAlaLeuAlaSerAspSerLysTrpProTrpGlnValSerLeuHisPheGlyThrThr 343
Db      775  GGCAGAGCGCGCTCCCGGGGCGCTGGCCCTGGCAGGTTCAGCTGCAGCTCCAGACGTC 834
Qy      344  HisIleCysGlyGlyThrLeuIleAspAlaGlnTrpValLeuThrAlaAlaHisCysPhe 363
Db      835  CACGTGTGCGAGGCTCCATCATCACCCCGAGTGTATCGTGCAGCGCCGCTCGGTG 894
Qy      364  PheValThrArgGlyLeuValLeuGly-----TrpLysValTyrAlaGlyThr 380
Db      895  -----GAATAACCTTTAAACATCCATGCGCATTTGAGCGCATTTGGCGGATT 942
Qy      381  SerAsnLeuHisGlnLeuProGluAlaAla-----SerIleAlaGluIleIleAsn 398
Db      943  TTGAGACAACTTTTCATCTTCTATGAGCGCGGATACCAAGTAGAAAGTAGTTCTCAT 1002
Qy      399  SerAsnTyrThrAspGluAspAspTyrAspIleAlaLeuMetArgLeuSerLysPro 418
Db      1003  CCAATTATGACTCCAGAGCAAGAACAAATGACATTTGCGCTGTATGAGCTGCAGAGCCT 1062
Qy      419  LeuThrLeuSerAlaHisIleProAlaCysLeuProMetHisGlyGlnThrPheSer 438
Db      1063  CTGACTTTCAACGACCTAGTAGAACACAGTGTCTGCCCAACCCAGGATGATGCTGCAG 1122
Qy      439  LeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThrAspLysThr 458
Db      1123  CCAGAACACTCTGTGTGATTTCGGGTGGGGGCCACCGAGGAG---AAAGGGAAGACC 1179
Qy      459  SerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAspTyr 478
Db      1180  TCAGAGTGTGAACGCTGCCAAGGTGTTCTCATTTGAGACACAGAGATGCAACAGCAGA 1239
Qy      479  LeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyGly 498
Db      1240  TATGCTATGACAACCTGATCACACAGCCATGATCTGTGCGGCTTCTTCAGGGGAC 1299
Qy      499  ArgAspSerCysGlnGlyAspSerGlyCysProLeuValCysGluGlnAsnAsnArgTrp 518
Db      1300  GTCGATTTCTCCAGGGTGACAGTGGAGGGCTCTGTGTCCTTCAGAGAACAAATATCTGG 1359
Qy      519  TyrLeuAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArgAsnLysProGlyVal 538
Db      1360  TGGCTGATAGGGGATACAGCTGGGTTCTGGCTGTGCCAAGCTTACAGACCCAGAGTG 1419
Qy      539  TyrThrLysValThrGluValLeuProTrpIleTyrSerLysMetGluSerGlu 556
Db      1420  TACGGGAATGTGTGTTATTACGAGCTGGATTTATCGACAAATGAGGGCAGAC 1473

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RESULT 3

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US-09-342-749-29
; Sequence 29, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TMRPS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 60/091,044
; EARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29

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; LENGTH: 2479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-342-749-29

Alignment Scores:
Pred. NO.: 7,75e-30
Score: 736.50
Percent Similarity: 47.40%
Best Local Similarity: 31.96%
Query Match: 24,56%
DB: 3

US-09-879-792-12 (1-562) x US-09-342-749-29 (1-2479)

Qy      27  AlaGlyThrProProGlyArgAla-----SerProAlaGln 38
Db      69  TCAGGGTCACCCACGACGCTATTGGACCTTACTATGAAACCATGGATACCAACCGAAAAAC 128
Qy      39  AlaSerProAlaGlnAlaSerProAlaGlyThrProProGlyArgAlaSerProAlaGln 58
Db      129  CCCTATCCCGCACAGCCACCTGTGTCCTCCCACT---GTCTACGAGGTGCTATCCGGCTCAG 185
Qy      59  AlaSerProAlaGlyThrProProGlyArgAlaSerProGlyArgAlaSerProAlaGln 78
Db      186  TACTATCCCGTCCCGCTGCTCC---CAGTACGCGCCCGAGGGTC 224
Qy      79  AlaSerProAlaArgAlaSerProAlaLeuAlaSerLeuSerArgSerSerSerGlyArg 98
Db      225  CTGACGAGGCT---TCCACCCCTGCTGTGACGAGCCCAATCCCATCCGG--- 278
Qy      99  SerSerSerAlaArgSerAlaSerValThrThrSerProThrArgValTyrLeuValArg 118
Db      279  -----ACAGTGTGCACCTCAAGACTAAGAAAGCACTGTGCATC 317
Qy      119  AlaThrProValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaThr 138
Db      318  ACCTTGACCTCGGGGACCTTC----- 338
Qy      139  ArgAlaThrArgGluSerProGlyThrSerLeuProLysPheThrTrpArgGluGln 158
Db      338  ----- 338
Qy      159  LysGlnLeuProLeuIleGlyCysValLeuLeuLeuIleAlaLeuValValSerLeuIle 178
Db      339  -----CTCGTGGGAGCT-----GGCTGGCGCTGGCTACTC 371
Qy      179  IleLeuPheGlnPheTrpGln-----GlyHisThrGlyIleArgTyr 192
Db      372  -----TGAAGTTTCATGGGCGACGAGTGTCTCAACTCTGGGATAGAGTGC 416
Qy      193  LysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValValAspCys 212
Db      417  ---GACTCTCTCAGGTACTGTGATCAACCCCTCTAACTGGTGTGATGGGTGTACACTGC 473
Qy      213  LysLeuLysSerAspGluLeuGlyCysValArgPheAspTrpAspLysSerLeuLeuLys 232
Db      474  CCGCGCGGGAGGACGAGATCGGTGTGTTCCTCTACGACCAAACTTCATCTCTCAG 533
Qy      233  IleTyrSerGlySerSerHisGlnTrpLeuProIleCysSerSerAsnTrpAsnAspSer 252
Db      534  ATGTACTCATCTCAGAGGAGTCTCTGGACCTCTGTGTCGACGACGACGACGAGAGAC 593
Qy      253  TyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThrGluVal 272
Db      594  TACGGCGGGCGGCTCGAGGACATGGCTATPAAGATAATTTTACTCTAGCCAA--- 650
Qy      273  AlaHisArgAspPheAlaAsnSerPheSerIleLeuArgTyrAsnSerThr----- 289
Db      651  GGAATAGTGGATGACAGCGGATCCACGAGCTTTATGAAACTGAACACACAGTCCGCGCAAT 710
Qy      290  -----IleGlnGluSerLeuHisArgSerGlu---CysProSerGlnArgTyrIleSer 306

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Db 711 GTCGATATCTATAAAAGCTGTACACAGTGATGCTGTTCTTCAAAAGCAGTGGTTCT 770
Qy 307 LeuGlnCysSerHisCysGlyLeuArg-----AlaMetThrGlyArgIleValGly 323
Db 771 TTACGCTGTTAGCCTGCGGGCTCAACTTGAACCTCAAGCGCCAGACGAGATGCTGGGC 830
Qy 324 GlyAlaLeuAlaSerAspSerIleValProTTPGlnValSerLeuHisPheGlyThr 343
Db 831 GGTGAGAGCGGCTCCCGGGGCGCTGCGCCCTGGCAGGTGAGCTGCAGTCCAGAACGTC 890
Qy 344 HisIleCysGlyGlyThrLeuIleAspAlaGlnTTPValLeuThrAlaAlaHisCysPhe 363
Db 891 CACGTGCGGAGGCTCCATCATCACCCCGAGTGGATGTCGACAGCGCCCTGCGGTG 950
Qy 364 PheValThrArgGluIleValLeuGluGly-----TTPlysValTyrAlaGlyThr 380
Db 951 -----GAAAAACCTCTTAACATCCATGCGCATTCGACGCGCATTTGCGGGATT 998
Qy 381 SerAsnLeuHisGlnLeuProGluAlaAla-----SerIleAlaGluIleIleAsn 398
Db 999 TTGACACATCTTCTGTTCTATGGAGCGGATACCAAGTACAAAAGTGAATTTCTCAT 1058
Qy 399 SerAsnTyrThrAspGluAspTyrAspIleAlaLeuMetArgLeuSerIleValPro 418
Db 1059 CCAAAATTATGACTCCAGACCAAGAACAAATGACATTCGCTGATGAAGCTGCAGAGCT 1118
Qy 419 LeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPheSer 438
Db 1119 CTGACTTTCAACAGACTAGTGAACAGTGTCTGTGCCCAACCCAGGCGATGATGTCGAG 1178
Qy 439 LeuAsnGlnThrCysTyrIleThrGlyPheGlyLysThrArgGluThrAspAspIleThr 458
Db 1179 CCAGAACAGCTCTGCTGATTTCCGGGTGGGGGGCCCGAGAG-----AAAGGGAAGACC 1235
Qy 459 SerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysCysAsnAspTyr 478
Db 1236 TCAGAAAGTGTGAACGCTGCCAAGTGTCTTCTCATTTGACACACAGATGCAACAGCAGA 1295
Qy 479 LeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyGly 498
Db 1296 TATGCTATGACAACTGATACACACAGCCATGATCTGTGCGGCTTCTGCGGGGAAC 1355
Qy 499 ArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGluGlnAsnAsnArgTrp 518
Db 1356 GTCGATTTTTCAGGGGTGACAGTGGAGGGGCTCTGGTCACTTCGAAACACAAATATCTGG 1415
Qy 519 TyrLeuAlaGlyValThrSerTTPGlyThrGlyCysGlyGlnArgAsnLysProGlyVal 538
Db 1416 TGGCTGATAGGGGATACAAAGCTGGGGTCTGGCTGTGCCMAAGCTTACAGACCGAGGTG 1475
Qy 539 TyrThrLysValThrGluValLeuProTTPIleTyrSerLysMetGluSer 555
Db 1476 TACGGGAATGTGATGGTATTACGAGCTGGATTATTCGACAAATGAAGGCA 1526
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RESULT 4

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US-09-691-840-29
; Sequence 29, Application US/09691840
; Patent No. 644419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: THPRS2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 29
; LENGTH: 2479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-691-840-29
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Alignment Scores:
Pred. No.: 7,75e-30 Length: 2479
Score: 736.50 Matches: 178
Percent Similarity: 47.40% Conservative: 86
Best Local Similarity: 31.96% Mismatches: 194
Query Match: 24.56% Indels: 99
DB: 4 Gaps: 18
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US-09-879-792-12 (1-562) x US-09-691-840-29 (1-2479)

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Qy 27 AlaGlyThrProGlyArgAla-----SerProAlaGln 38
Db 69 TCAGGTGTACACACAGCTATTGGACCTTACTATGAAAAACCATGGATACCAACCGGAAC 128
Qy 39 AlaSerProAlaGlnAlaSerProAlaGlyThrProGlyArgAlaSerProAlaGln 58
Db 129 CCTATCCGACACAGCCCACTGTGTCCCACT---GTCACGAGGTGATCGGCTCAG 185
Qy 59 AlaSerProAlaGlyThrProGlyArgAlaSerProGlyArgAlaSerProAlaGln 78
Db 186 TACTACCGGTCCCGCGTGCCTC-----CAGTACGCCCGGAGGTC 224
Qy 79 AlaSerProAlaArgAlaSerProAlaLeuAlaSerLeuSerArgSerSerSerGlyArg 98
Db 225 CTGACGCGAGCT---TCCAAACCCCTGCTGTCACGAGCCCAAAATCCCATCCGCG--- 278
Qy 99 SerSerSerAlaArgSerAlaSerValThrThrSerProThrArgValTyrLeuValArg 118
Db 279 -----ACATGTGCACCTCAAGACTAAGAACACTGTGCATC 317
Qy 119 AlaThrProValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaThr 138
Db 318 ACCTTGACCTCGGGGACCTTC----- 338
Qy 139 ArgAlaThrArgGluSerProGlyThrSerLeuProLysPheThrTyrArgGluGlyGln 158
Db 338 ----- 338
Qy 159 LysGlnLeuProLeuIleGlyCysValLeuLeuLeuIleAlaLeuValSerLeuIle 178
Db 339 -----CTCGTGGAGCT-----GCCTGGCCGCTGCTACTC 371
Qy 179 IleLeuPheGlnPheTyrGln-----GlyHisThrGlyIleArgTyr 192
Db 372 -----TGAAGTTTCATGGGCGAGAGTGTCTCCAACTCTGGGATAGAGTGC 416
Qy 193 LysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValValAspCys 212
Db 417 ---GACTCCTCAGGTACCTGTCATCAACCCCTCTAATCTGGTGTGATGGCGGTGCACACTGC 473
Qy 213 LysLeuLysSerAspGluLeuGlyCysValArgPheAspTyrAspLysSerLeuLeuLys 232
Db 474 CCGCGCGGGAGGACGAGAAATCGGTGTGTTTGCCTCTACGACCAAACTTCACTCTTCAG 533
Qy 233 IleTyrSerGlySerSerHisGlnTyrLeuProIleCysSerSerAsnTyrAsnAspSer 252
Db 534 ATGTACTCATCTCAGAGGAAGTCTCTGCACCTGTGTGCCAAGACGACTGGAACGAGAAC 593
Qy 253 TyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThrGluVal 272
Db 594 TACGGCGGGCGCGCTGCAGGGACATGGGCTATAGATATATTTTACTCTAGCCAA--- 650
Qy 273 AlaHisArgAspPheAlaAsnSerPheSerIleLeuArgTyrAsnSerThr----- 289
Db 651 GGAATAGTGGATGACGCGGATCCACGAGCTTTATGAACACTGAACACAGGTGCGCGCAAT 710
Qy 290 -----IleGlnGluSerLeuHisArgSerGlu---CysProSerGlnArgTyrIleSer 306
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Db 711 GTCGATATCTATAAAACCTGTACACAGTGATGCTGTCTTCAAAGCAGTGGTTCT 770
QY 307 LeuGlnCysSerHisCysGlyLeuArg-----AlaMetThrGlyArgIleValGly 323
Db 771 TTACGCTGTTTACCTCGCGGGTCACTTGAATCAAGCCGACAGCAGATCGTGGGC 830
QY 324 GlyAlaLeuAlaSerAspSerLysTyrProTyrGlnValSerLeuHisPheGlyThr 343
Db 831 GGTGAGAGCGCGCTCCCGGGGGCTGGCCCTGGCAGGTCAAGCTGCACGTCACGAAGTC 890
QY 344 HisIleCysGlyGlyThrLeuIleAspAlaGlnTyrValLeuThrAlaAlaHisCysPhe 363
Db 891 CAGGTGCGAGGCTCCATCATCAACCCGAGTGGATCGTACAGCCGCCACTGGTG 950
QY 364 PheValThrArgGluLysValLeuGluGly-----TyrLysValTyrAlaGlyThr 380
Db 951 -----GAAAAACCTCTTAAACATCCATGGCATTTGGACGGCATTTGGGGATT 998
QY 381 SerAsnLeuHisGlnLeuProGluAlaAla-----SerIleAlaGluIleIleAsn 398
Db 999 TTGAGCAATCTTTTCATGTTCTATGGAGCCGGATACCAAGTACAAAAAGTATTTCTCAT 1058
QY 399 SerAsnTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArgLeuSerLysPro 418
Db 1059 CCAATTATGACTCCAGACCAAGACAATGATTCGCTGATGAGCTGCGAAGCCCT 1118
QY 419 LeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPheSer 438
Db 1119 CTGACTTTCAACGACCTAGTGAACCAAGTGTGTCTGCCCAACCCAGGCATGATGTCGAG 1178
QY 439 LeuAsnGluThrCysThrPheThrGlyPheGlyThrArgGluThrAspLysThr 458
Db 1179 CCGAAGACCTCTGCTGGATTTCCGGGTGGGGGCCACCGAGGAG---AAAGGAAGACC 1235
QY 459 SerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAspTyr 478
Db 1236 TCAGAAGTGTGAACCTGCAAGGTGCTTCTCATTTGAGACACAGATGCAACACAGA 1295
QY 479 LeuValTyrAspSerTyrThrThrProArgMetMetCysAlaGlyAspLeuArgGly 498
Db 1296 TATGCTATGACAAACCTGATCACACGACCATGATCTGTGCGGCTTCTGCGAGGGGAAC 1355
QY 499 ArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGluGlnAsnAsnArgTyr 518
Db 1356 GTGCTATCTTCCAGGTGACAGTGGAGGCGCTCTGCTCACTTCGAACCAACAATATCTCG 1415
QY 519 TyrLeuAlaGlyValThrSerTyrGlyThrGlyCysGlyGlnArgAsnLysProGlyVal 538
Db 1416 TGGCTGATAGGGGATACAAAGCTGGGGTCTGGCTGTGCCAAGCTTACAGACCAAGGATG 1475
QY 539 TyrThrLysValThrGluValLeuProTyrPheTyrSerLysMetGluSer 555
Db 1476 TACGGGAATGTGATGTATTACGGGACTGGATTTATCGACAAATGAAGCA 1526
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RESULT 5

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US-09-518-046-1
; Sequence 1, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 1
; LENGTH: 2413
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 gene
US-09-518-046-1
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Alignment Scores:
Pred. No.: 2,19e-29 Length: 2413
Score: 727.50 Matches: 170
Percent Similarity: 49.70% Conservative: 79
Best Local Similarity: 33.93% Mismatches: 193
Query Match: 24.26% Indels: 59
DB: 3 Gaps: 13
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US-09-879-792-12 (1-562) x US-09-518-046-1 (1-2413)

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QY 107 ValThrThrSerProThrArgValTyrLeuValArgAlaThrProValGly----- 123
Db 30 GTAACACTGTGGCTACTATCTCTCCGTGGTGCCATCTACATTTTGGGACTCGGGAAT 89
QY 124 ---AlaValProIleArgSerSerProAlaArgSerAlaPro-----AlaThrArgAla 140
Db 90 TATGAGGTAGAGTGGGCGGCGGATGTCAGAGTCTCTGAAATAGTCAACATGGGG 149
QY 141 ThrArgGluSerProGlyThrSerLeuProLysPheThrTrpArg----- 155
Db 150 GAAATGATCGCGCTCTGTGTAAGCCCC---TTCTCATTCGATCGCTTTTGGCCTT 206
QY 155 ----- 155
Db 207 GATGATTGAAATAAGTCTCTGTTCACACAGATGCTGTCTGTCACAGATCCTCTG 266
QY 156 -----GluGlyGlnLysGlnLeuProLeuIleGlyCysValLeuLeuLeu 170
Db 267 TCACCTGCTGCCATTGAGTGTTCCTCAATCATCTCATTCGGGATCATTCGATGATA 326
QY 171 IleAlaLeuValSerLeuIleLeuPheGlnPheTrpGlnGlyHisThrGlyIle 190
Db 327 TTAGCACTGCCATTGGTCTGGGCATCCACTTCGACTGC-----TCAGGGAAG 374
QY 191 ArgTyrLysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValVal 210
Db 375 TACAGATGTCGTCAATCTTAAAGTGTATCGAGCTGATAACTCGATGTACGAGTCTCG 434
QY 211 AspCysLysLeuLysSerAspGluLeuGlyCysValArgPheAspTrpAspLysSerLeu 230
Db 435 GATTGCAAGACAGCGGAGGACAGTACCGCTGTGTCGGGTGGTGGTGCAGATGCGGTG 494
QY 231 LeuLysIleTyrSerGlySerSerHisGlnTrpLeuProIleCysSerSerAsnTrpAsn 250
Db 495 CTCAGGTGTTCCACAGCTGCTTCG-----TGAAGACCATGTGCTCCGATGACTGGAAG 548
QY 251 AspSerTyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThr 270
Db 549 GGTCACTAGCAAAATGTTCCTGTCCTCCCACTGGGTTTCCCAAGCTATGTGATGTCAGAT 608
QY 271 GluValAla-----HisArgAspPheAlaAsnSerPheSer 282
Db 609 AACCTCAGATGAGTCTGCTGGAGGGGAGTTCGGGAGGAGTTCGTGTCATCGATCAC 668
QY 283 IleLeuArgTyrAsn-----SerThrIleGlnGluSerLeuHis---ArgSerGluCys 299
Db 669 CTCCTGCCAGATGACACAGGTGATGCAATTACACCACTCAGTATATGTGAGGGAGGATGT 728
QY 300 ProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGly---LeuArgAlaMetThr 318
Db 729 GCCTCTGCCACGTGTTACCTTGCAGTGCACAGCCTGTGGTTCATAGAAGGGGGCTACAGC 788
QY 319 GlyArgIleValGlyValAlaLeuSerAspSerLysTrpProTyrGlnValSerLeu 338
Db 789 TCAGCATCGTGGTGGAAACATGTCCTTCTCGCAGTGGCCCTGCGACGCCACCTT 848
QY 339 HisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGlnTrpValLeuThr 358
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Db 849 CAGTTCAGGGCTACACCTGCGGGGCTGTGTCATCAGCCCTGTGGATCATCACT 908
 QY 359 AlalaHisCysPheValThrArgGluValLeuGluGlyTrpLysValTyrAla 378
 Db 909 GCTGCACACTGTGTATGACTTG-----TACCTCCCAAGATCATGACCATCCAGGTTG 962
 QY 379 GlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGlu---IleIleIle 397
 Db 963 GGTCTAGTTCCCTGTGGCAATCAGCCCAATCCCACTGTGTGGAGAGATGTCTAC 1022
 QY 398 AsnSerAsnTyrThrAspGluGluAspAspTyrAspIleAlaLeuMetArgLeuSerLys 417
 Db 1023 CACAGCAAGTACAAGCCAAAGAGCTGGGCAATGACATGCCCTTATGAAGCTGGCGGG 1082
 QY 418 ProLeuThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPhe 437
 Db 1083 CCATCACTCAATGAATAATGATCCAGCCTGTGTGCTGCCCACTCTGAAGAGAACTTC 1142
 QY 438 SerLeuAsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThrAspAspLys 457
 Db 1143 CCCGATGAAAAGTGTCTGACGTCAAGATGGGGGCCACAGAGGATGGAGGTGAC--- 1199
 QY 458 ThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAsp 477
 Db 1200 GCCTCCCTCTGCTGAAACACACGCGCGCTCCCTTGTATTCACCAAGATCTGCACACC 1259
 QY 478 TyrLeuValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGly 497
 Db 1260 AGGACGTGTACGGTGCATCACTCCCTCCCTCCATGCTGTGCGGGGCTACCTGACGGGT 1319
 QY 498 GlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysGluGlnAsnAsnArg 517
 Db 1320 GCGGTGAACAGCTGCCAGGGGAGCAGCGGGGGGCGCTGGTGTGTCAAGAGAGGCGTG 1379
 QY 518 TrpTyrLeuAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArgAsnLysProGly 537
 Db 1380 TGGAGTTAGTGGAGGACGACGCTTTGGCATGCGCTGCCAGAGTGAACAGCTGGG 1439
 QY 538 ValTyrThrLysValThrGluValLeuProTrpIleTyrSerLysMetGluSerGluVal 557
 Db 1440 GTGTACACCGGTGTCACTCTCTCTGACTGGATCCAGCAGCAGATGGAGAGAGACCTA 1499
 QY 558 Arg 558
 Db 1500 AAA 1502

RESULT 6

US-09-656-002-1
 ; Sequence 1, Application US/09656002
 ; Patent No. 6455668
 ; GENERAL INFORMATION:
 ; APPLICANT: Mack, David
 ; APPLICANT: Gish, Kurt
 ; APPLICANT: Wilson, Keith
 ; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND
 ; TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
 ; FILE REFERENCE: A-69108/DIB/JJD/AMS
 ; CURRENT APPLICATION NUMBER: US/09/656,002
 ; CURRENT FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: US 09/525,993
 ; PRIOR FILING DATE: 2000-03-15
 ; PRIOR APPLICATION NUMBER: US 09/493,444
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: PCT/US 00/07044
 ; PRIOR FILING DATE: 2000-03-15
 ; NUMBER OF SEQ ID NOS: 3
 ; SEQ ID NO 1
 ; LENGTH: 2079
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-656-002-1

Alignment Scores:
 Pred. No.: 1,04e-28 Length: 2079
 Score: 713.00 Matches: 180
 Percent Similarity: 48.08% Conservations: 83
 Best Local Similarity: 32.91% Mismatches: 212
 Query Match: 23.77% Indels: 74
 DB: 4 Gaps: 15
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 Db 6 GCAGCAGCTTGTTCAGCGCAGCAGGATCTGGGGGTGAGGACCAAGGCTTGCCT-GCA 64
 QY 62 AlaglyThrProGlyArgAlaSerProGlyArgAlaSer-----ProAlaGlnAla 79
 Db 65 CTCGGGCTCTCTCCAGCCAGCTGCTGACCCAGGACTTCTGACCTGTGCTCCAGCAGGACC 124
 QY 80 SerProAlaArgAlaSerProAlaLeu---AlaSerLeuSerArg-SerSerSerGlyAr 98
 Db 125 TGTGTGGGGAGGCGCTCTCTGCTGCTGGGGTGCACATCTCAGCTCCAGGCTCAGGGAG 184
 QY 98 gSerSerSerAlaArgSerAlaSerValThrSerProThrArgValTyrLeuValAr 118
 Db 185 ACCGGGAGGATCACAGAGCCAGCATGTGTACAGGATCTCTG-ACAGTGATCACTCTGAAC 243
 QY 118 gAlaThrProValGlyAlaValProIleArgSerSerProAlaArgSerAlaProAlaTh 138
 Db 244 AGCTCTG-----ATGTCAAACCCCTCGCCAAAC----- 271
 QY 138 rArgAlaThrArgGluSerProGlyThrSerLeuProLysPheThrTrpArgGluGlyGl 158
 Db 272 -----CCCGTATATCCCATGTGGAGACTTCATCATTTGTGTGT 297
 QY 158 nLys---GlnLeuProLeuIleGlyCysValLeuLeuLeuIleAlaLeuValSerLe 177
 Db 298 AAGTGTGGGATCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTTGTGTGT 357
 QY 177 uIleIleLeu-----PheGlnPheTrpGlnGlyHisThrGlyIleAr 191
 Db 358 TGTCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTCTCGCGGCGAG----- 406
 QY 191 gTyrLysGluGlnArgGluSerCysProLysHisAlaVal-----ArgCysAs 207
 Db 407 -----CCTCTCCACTTTCATCCCGAGGAGAGAGCTGTGTGA 441
 QY 207 pGlyValValAspCysLysLeuLysSerAspGluLeuGlyCys----- 221
 Db 442 CGGAGAGCTGGACTGTCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCGA 501
 QY 222 -----ValArgPheAspTrpAspLysSerLeuLeuLysIleTyrSerGl 236
 Db 502 AGGGCTCTGCAGTGGCAGTCCGCTCTCCAAGACCGCATCCACATGCAAGTGTGACTC 561
 QY 236 ySerSerHisGlnTrpLeuProIleCysSerSerAsnTrpAsnAspSerTyrSerGluY 256
 Db 562 GCGCACAGGAACTGTCTCTGCTCTGCTGCTTTCGACAACTTTCACAGAGCTTCGCTGAGAC 621
 QY 256 sThrCysGlnGlnLeuGlyPheGluSer-----AlaHisArgThrThrGluValAlaHi 274
 Db 622 AGCCTGTAGGACAGATGGGTACAGCAGCAAAACCCACTTTCAGAGCTGTGGAGATTGGCCC 681
 QY 274 sArgAspPheAlaAsnSerPheSerIleLeuArgTyrAsnSerThrIleGlnGluSerLe 294
 Db 682 AGACCAGGATCTGGATGTGTGTAATCACAGAAACACAGGAGGCTTTCGATCGCGAA 741
 QY 294 uHisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLe 314
 Db 742 CTCAGTGGGCGCTGTCTCTCAGGCTCCCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 801
 QY 314 uArgAlaMetThrGlyArgIleValGlyAlaLeuAlaSerAspSerLysTrpProTr 334

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Db 802 GAGCCTGAACACCCCGTGTGGTGGGAGGAGCCCTCTGTGATTCCTGGCCCTTG 861
QY 334 pGlnValSerLeuHisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGl 354
Db 862 GCAGGTGAGCATCCAGTACACAAACAGCAGCAGTCTGTGGAGGAGCATCTCGACCCCA 921
QY 354 nTTPValLeuThrAlaAlaHisCysPhePheValThrArgGluLysValLeuGluGlyTr 374
Db 922 CTGGTCTCAGCGCAGCCCTGCTTC-----AGGAACATACACCATGTTCAACTG 975
QY 374 pLysValTyrAlaGlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGl 394
Db 976 GAAGGTGCGGCGAGGCTCAGACAACTGGCAGCTCCCATCCCTGCTGCT---GTGGCAA 1032
QY 394 uIleIleIle-----AsnSerAsnTyrThrAspGluLysAspPyrAspIleAl 411
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QY 411 aLeuMetArgLeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeuPr 431
Db 1084 CCTCATGAGCTGAGTTCCTCCACTCTCTCAGGCACAGTCAGGCCCATCTGTCTGCC 1143
QY 431 oMetHisGlnThrPheSerLeuAsnGluThrCysfTrpIleThrGlyPheGlyLysTh 451
Db 1144 CTTCCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGCTTAC 1203
QY 451 rArgGluThrAspAspLysThrSerProPheLeuArgGluValGlnValAsnLeuIleAs 471
Db 1204 GAAGCAGATGGAGGGAAGATGTCTGACATCTGCTGCAGGCGTCAGTCAGTCTTGA 1263
QY 471 pPheLysLysCysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMetMetCy 491
Db 1264 CAGCACACGGTGCATTCAGACAGCATCGTACACAGGGGGAGTCCACGAGAGATGATGT 1323
QY 491 sAlaGlyAspLeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeuVa 511
Db 1324 TGCAGGCATCCCGAAGGGGGTGTGGACACCTCCAGGGGTGACAGTGGTGGGCCCTGAT 1383
QY 511 lCysGluGlnAsnAsnArgTyrTyrLeuAlaGlyValThrSerTyrGlyThrGlyCysGl 531
Db 1384 G---TACCATCTGACCGAGGCGATGTGTGGCGATCGTTAGTGGGGCTATGGCTGCGG 1440
QY 531 yGlnArgAsnLysProGlyValTyrThrLysValThrGluValLeuProTyrTrpSer 551
Db 1441 GGCGCCGAGCACCCAGGAGTATACACCAAGTCTCAGCCTATCTCACTGGATCTACAA 1500
QY 551 rLysMetGluSerGluVal 557
Db 1501 TGTCTGGAGGCTGAGCTG 1519
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RESULT 7

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US-09-518-046-3
; Sequence 3, Application US/09518046
; Patent No. 6294663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
; FILE REFERENCE: D6192CIP
; CURRENT APPLICATION NUMBER: US/09/518,046
; CURRENT FILING DATE: 2000-03-02
; EARLIER APPLICATION NUMBER: 09/261,416
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 3
; LENGTH: 2544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: entire cDNA sequence of TADG-12 variant gene
US-09-518-046-3
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Alignment Scores:

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Pred. No.: 2,36e-28 Length: 2544
Score: 708.00 Matches: 175
Percent Similarity: 46.78% Conservative: 79
Best Local Similarity: 32.23% Mismatches: 190
Query Match: 23.61% Indels: 100
DB: 3 Gaps: 15
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US-09-879-792-12 (1-562) x US-09-518-046-3 (1-2544)

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Db 30 GTAACACTGTGGCTACTATCTCTCCGTGGTGCCTACATTTTGGGACTCGGGAAAT 89
QY 124 ---AlaValProIleArgSerSerProAlaArgSerAlaPro-----AlaThrArgAla 140
Db 90 TATGAGGTAGAGTGGGCGGAGCGCGATGTCTCAGAGGTCTCTGAATAGTCACCATGGGG 149
QY 141 ThrArgGluSerProGlyThrSerLeuProLysPheThrTrpArg----- 155
Db 150 GAAATGATCGGCTGCTGTGTGAAGCCCG---TTCATTCGATCGCTTTTGGGCTT 206
QY 155 ----- 155
Db 207 GATGATTGAAATAAGTCTCTGTGCACGAGATGCAGATGCTGTGTCGACAGATCTCTG 266
QY 156 -----GluGlyGlnLysGlnLeuProLeuIleGlyCysValLeuLeuLeu 170
Db 267 TCACCTCTGCCATTGAGTGTTCCTCAATCATCTCATTTGGGGATCATTTGATTTGATA 326
QY 171 IleAlaLeuValSerLeuIleLeuPheGlnPheTrpGlnGlyHisThrGlyIle 190
Db 327 TTAGCAGTCGGCATCTGCTGGGCATCCACTTCGACTGC-----TCAGGGAAG 374
QY 191 ArgTyrLysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValVal 210
Db 375 TACAGATGCTCATCTTTTAAAGTGTATCGAGCTGATTAATCTGATGTGCGGAGTCTCG 434
QY 211 AspCysLysLeuLysSerAspGluLeuGlyCysValArgPheAspTrpAspLysSerLeu 230
Db 435 GATTGCAAGAGCGGGAGACGAGTACCCCTGTGTCGGTGGTGGTGGTGGTGGTGGTGG 494
QY 231 LeuLysIleTyrSerGlySerSerHisGlnTrpLeuProIleCysSerSerAsnTrpAsn 250
Db 495 CTCAGGTGTTACAGCTGCTTCG-----TGAAAGCCATGTGCTCCGATGATGGAAG 548
QY 251 AspSerTyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThr 270
Db 549 GGTCTACTAGCAAAATGTTGCTGTCGTCGCAACTGGGTTTCCCAAGCTATGTAAAGTTCAGAT 608
QY 271 GluValAla-----HisArgAspPheAlaAsnSerPheSer 282
Db 609 AACCTCAGAGTGTGCTGCTGAGGGGCGAGTTCCGGGAGGAGTTTGTGTCATCGATCAC 668
QY 283 IleLeuArgTyrAsn-----SerThrIleGlnGluSerLeuHis---ArgSerGluCys 299
Db 669 CTCCTTGCAGATGACAAAGGTGACTGCATTTACACCACTCAGTATATGTGAGGAGGATGT 728
QY 300 ProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGly---LeuArgAlaMetThr 318
Db 729 GCCTCTGGCCAGCTGGTTACCTTGCAGTGCACAGCCTGTGGTGCATAGAGGGGCTACAGC 788
QY 319 GlyArgIleValGlyValAlaLeuAlaSerAspSerLysTrpTrpTrpGlnValSerLeu 338
Db 789 TCACGCATCTGGTGGTGGAAACATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848
QY 339 HisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGlnTrpValLeuThr 358
Db 849 CAGTTCCAGGGCTACCACTGTGGGGGGCTCTGTGTCATCACGCCCTCTGTGATCATCACT 908
QY 359 AlaAlaHisCysPhePhe-----ValThrArgGluLysVal----- 370
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QY	211	spCyalsysLeuIysSerAspGluLeuGlyCys	-----	221
DB	438	ACTGTCCTTTGGGGAGACGAGGACACTGTGTCAAGAGCTTCCCGAAGGCCCTGCCAG	497	
QY	222	-----ValArgPheAspTrpAspIysSerLeuLeuIysIleTySerGlySerSerHisG	240	
DB	498	TGGCAGTCCCGCTCTCCAAAGACCGATCCACATCGCAGGTGCTGGACTCGGCCACGGA	557	
QY	240	InTrpLeuProIleCySerSerAsnTrpAsnAspSerTySerGluIysTrpCyAsGlnG	260	
DB	558	ACTGGTTCTCTGCCTGTTTCGACAACTTCACAGAGCTCTCGCTGAGACAGCCTGTAGGC	617	
QY	260	InLeuGlyPheGluSer-----AlaHisArgThrThrGluValAlaHisArgAspPheA	278	
DB	618	AGATGGGCTACAGCAGCAAAACCCACTTTCAGAGCTGTGGAGATGTGGCCACGACCAGATC	677	
QY	278	laAsnSerPheSerIleLeuArgTyArgAsnSerThrIleGlnGlnSerLeuHisArgSerG	298	
DB	678	TGGATGTTGTGAATACAGAAACAGCCAGGAGCTTCGCATCGCGAACTCAAGTGGGC	737	
QY	298	luCySerProSerGlnArgTyIleSerLeuGlnCySerHisCyGlyIysValArgAlaMet	318	
DB	738	CCTGTCTCTCAGGTCCTCGCTGCCCTGCATCTCTTGCCTGTGGGAGAGCCTCGAAGA	797	
QY	318	hrGlyArgIleValGlyAlaLeuAlaSerAspSerTySerTrpTrpGlnValSerL	338	
DB	798	CCCCCGTGTGGTGGGAGGAGCCCTCTGTGGATTCTTGGCTTGGCAGTGCAGCA	857	
QY	338	euHisPheGlyThrThrHisIleCyGlyGlyThrLeuIleAspAlaGlnTrpValLeuT	358	
DB	858	TCCAGTAGCAGCAAAACAGCACGTCGTGGAGGAGCATCCTGGACCCCCACTGGGTCTCA	917	
QY	358	hrAlaAlaHisCyPhePheValThrArgGluIysValLeuGluGlyTrpIysValTyAr	378	
DB	918	CGGCAGCCCACTGCTTC-----AGGAAACATACCGATGTGTTCAACTGGAAGTGGCG	971	
QY	378	laGlyThrSerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGluIleIleLe-	397	
DB	972	CAGGCTCAGACAAACTGGGCGAGCTTCCATCCCTGGCT---GTGGCCAAATCATCATCA	1028	
QY	398	-----AsnSerAsnTyThrAspGluGluAspAspTyAspIleAlaLeuMetArgL	415	
DB	1029	TTGAATTCAA CCCCATGTAC-----CCCAAGACATGATCATCGCCTCATGAGC	1079	
QY	415	euSerLysProLeuThrLeuSerAlaHisIleHisProAlaCyGluLeuProMetHisGlyG	435	
DB	1080	TGCAGTTCCTCCACTCATTCTTCAGGCACAGTCAGGCCCATCTGTCTGCCCTCTTTGATG	1139	
QY	435	InThrPheSerLeuAsnGluThrCysTrpIleThrGlyPheGlyIysThrArgGluThrAr	455	
DB	1140	AGGAGTCACTCCAGCCACCCTCTGGATCATTTGGATGGGCTTTACGAGCAGAGATG	1199	
QY	455	spAspLysThrSerProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysC	475	
DB	1200	GAGGGAAGATGCTGCACATCTGCTGCAGGCGTCAGTCCAGTCAATTGACAGCACACGT	1259	
QY	475	ysAsnAspTyIleuValTyArgSerTyLeuThrProArgMetMetCysAlaGlyAspL	495	
DB	1260	GCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAGATGATGTGTGAGGCATCC	1319	
QY	495	euArgGlyIysArgAspSerCysGlnGlyAspSerGlyIysProLeuValCysGluGlnA	515	
DB	1320	CGAAAGGGGGTGTGACACCTTCCTCCAGGTGACAGTGGTGGGCCCTCATG---TACC	1376	
QY	515	snAsnArgTrpTyLeuAlaGlyValThrSerTrpGlyThrGlyCyGlyGlnArgAsnL	535	
DB	1377	CTGACCAATGGCATGTGTGGGCATCGTGTAGTGGGCTATGTGGTGGGGGCCCGACGA	1436	
QY	535	ysProGlyValTyThrLysValThrGluValLeuProTrpIleTySerLysMetGluS	555	
DB	1437	CCCCAGGAGTATACACCAAGGTCTCAGGCTATCTCAACTGATCTTCAACTCTCTGGAGG	1496	

Qy 555 erGluVal 557
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Db 1497 CTGAGCTG 1504

RESULT 9
US-09-261-416-1
; Sequence 1, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TAGD-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 144..1511
; OTHER INFORMATION: CDS
US-09-261-416-1

Alignment Scores:
Pred. No.: 1,11e-27 Length: 2416
Score: 694.50 Matches: 170
Percent Similarity: 49.21% Conservative: 78
Best Local Similarity: 33.73% Mismatches: 194
Query Match: 23.16% Indels: 62
DB: 3 Gaps: 13

US-09-879-792-12 (1-562) x US-09-261-416-1 (1-2416)

Qy 107 ValThrThrSerProThrArgValTyrLeuValArgAlaThrProValGly----- 123
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Db 30 GTAACACTGTGGCTACTATCTCTTCGTGTGTGCATCTACATTTTGGGACTCGGGAA 89
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Qy 124 --AlaValProIleArgSerSerProAlaArgSerAlaPro-----AlaThrArgAla 140
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Db 90 TATGAGGTAGAGGTGGAGCGGAGCGGATGTCAGAGTCTGAAATAGTCACCATGGG 149
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Qy 141 ThrArgGluSerProGlyThrSerLeuProLysPheThrTrpArg----- 155
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Db 150 GAAATGATCGCGCTGCTGTGTGAAGCCCC--TTCTCATTCGATCGCTTTTGGCCTT 206
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Qy 155 ----- 155

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Qy 171 IleAlaLeuValSerLeuIleLeuPheGlnPheThrGlnGlyHisThrGlyLe 190
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Db 327 TTAGCACTGGCCATTGGTCTCGGCATCCACTTCGACTGC-----TCAGGGAG 374
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Qy 191 ArgTyrLysGluGlnArgGluSerCysProLysHisAlaValArgCysAspGlyValVal 210
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Db 375 TACAGATGCTGCTCATCTTTAAGTGTATTCGAGCTGATAAATCTGATGTGACGGAGTCTCG 434
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Qy 211 AspCysLysLeuLysSerAspGluLeuGlyCysValArgPheAspTrpAspLysSerLeu 230
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Db 435 GATTGCAAGACGGGGAGGACGAGTAGCCGCTGTGTCCGGGTGGGTGTGCAGAAATGCCGTG 494
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Qy 231 LeuLysIleTyrSerGlySerSerHisGlnTrpLeuProLysCysSerSerAspTrpAsn 250
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Qy 251 AspSerTyrSerGluLysThrCysGlnGlnLeuGlyPheGluSerAlaHisArgThrThr 270
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Db 357 -----GCCATTGTGGCTGTTCTCTCAGGAGTGACCGAGCGCGTG 398
Qy 220 GlyCysValArgPheAspTrpAspIysSerLeuLeuYleTyrSerGlySerSerHis 239
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Qy 240 GlnTrpLeuProIleCysSerSerAsnTrpAsnAspSerTyrSerGluYlsThrCysGln 259
Db 459 ACCTGGCGGCTGCTGCTCTCTCGGCTCAAGCCAGCGGTAGCGAGCTCAGCTCGCAG 518
Qy 260 GlnLeuGlyPheGlnSerAlaHisArgThrThrGluValAlaHisArgAsp 276
Db 519 GAGATGGCTCTCTCAGGCGACTGACCCATCCGAGCTGAGCGTGCAGAGCGCGCGCC 578
Qy 277 -----PheAlaAsnSerPheSerIleLeuArgTyrAsnSerThrIle 290
Db 579 AATGGCAGCTCGGGCTTCTCTGTGGACGAGGGAGGCTGCCCCACACCCAGAGGTG 638
Qy 291 GlnGluSerLeuHisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSer 310
Db 639 CTGAGGTATCTCCGTGTGTGATGTCGCCAGAGGCGGTTCTTGCGCGCCATCTGCCAA 698
Qy 311 HisCysGlyLeuArgAlaMet---ThrGlyArgIleValGlyGlyValAlaSerAsp 329
Db 699 GACTGTGGCGCGAGAGCTGCCCGTGGACCGCATCTGTGGAGCGCGGACACCGAGTGG 758
Qy 330 SerLysTrpProTrpGlnValSerLeuHisPheGlyThrThrHisIleCysGlyGlyThr 349
Db 759 GGCGGTGGCGGTGGCAAGTCAGCTTCGTATGATGGAGCACACCTCTGTGGGGATCC 818
Qy 350 LeuIleAspAlaGlnTrpValLeuThrAlaAlaHisCysPhePheValThrArgGluYls 369
Db 819 CTGCTCTCCGGGAGCTGGGTGTGTGACAGCGCGCCACTGC---TTCGCGAGCGGAACCGG 875
Qy 370 ValLeuGluGlyTrpLysValTyrAlaGlyThr-----SerAsnLeuHisGlnLeu 386
Db 876 GTCTCTCCGATGGCGAGGTGTTGCGGTGGCGGTGGCGCGCGCTCTCCACAGGTCTG 935
Qy 387 ProGluAlaAlaSerIleAlaGluIleIleAlaSerAsnTyr----- 401
Db 936 -----CAGCTGGGGGTGAGGCTGTGGTCTACACGCGGGGTATCTTCCCTTTCGGGAC 989
Qy 402 ---ThrAspGluAlaAspTyrAspIleAlaLeuMetArgLeuSerLysProLeuThr 420
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Qy 461 PheLeuArgGluValGlnValAlaLeuIleAspPheLysLysCysAsnAspTyrLeuVal 480
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Qy 481 TyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyGlyArg 500
Db 1227 TATGGAACACAGATCAAGCCCAAGATGTTCTGTGCTGGCTACCCCGAGGCTGCAATGAT 1286
Qy 501 SerCysGlnGlyAspSerGlyProLeuValCysGlu-----GlnAsnAsn 516
Db 1287 GCCTGCCAGCGGCGACAGCGGTGTCTCTTGTGTGTGAGGACAGCATCTCTCGAGCGCA 1346
Qy 517 ArgTrpTyrLeuAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArgAsnLysPro 536
Db 1347 CGTTGGCGGCTGTGTGCAATTGTGAGTGTGGGCACTGGCTGTGCTGCCCGCCAGAGCCA 1406
Qy 537 GlyValTyrThrLysValThrGluValLeuProTrpIleTyrSerLysMetGluSer 555
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RESULT 12

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US-09-861-966-188
; Sequence 188, Application US/09861966
; Patent NO. 6518028
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A/Div
; CURRENT APPLICATION NUMBER: US/09/861,966
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 09/510,738
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 188
; LENGTH: 1783
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length cDNA of hepsin
US-09-861-966-188
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Alignment Scores:
Score: 3.84e-25 Length: 1783
Percent Similarity: 642.50 Matches: 170
Best Local Similarity: 46.01% Conservative: 78
Query Match: 31.54% Mismatches: 203
Indels: 89
Gaps: 17
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US-09-879-792-12 (1-562) x US-09-861-966-188 (1-1783)

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Db 1 TCGAGCCCGCTTTCAGGAGCCCTTCTCTGAGGGCCACAGTGGCA----- 48
Qy 74 AlaSerProAlaGlnAlaSerProAlaGlyThrProGlyArgAlaSerProAlaGly 93
Db 49 -----GCCTGGCTTAGAGGCCCCAC---GCCACCGCTCTGCTCCAGG 90
Qy 94 SerSerSerGlyArgSerSerSerAlaArgSerAlaSerValThrThrSerProThrArg 113
Db 91 CCGCCCGCTGTCTGGGGGCGCCACCATGTCTCTGCCAGGCTGGAGACTGACCGGCC--- 147
Qy 114 ValTyrLeuValArgAlaThrProValGlyAlaValProIleArgSerSerProAlaArg 133
Db 148 -----CCGGCACTACTCTGAGGCTCCGCGGCTCCGCGGCTGCTGAGACCCAGGCTCC 195
Qy 134 SerAlaProAlaThrArgAlaThrArgGluSer-----ProGlyThrSerLeuProLys 151
Db 196 CACCTGTG-CCAGAGGTGACCGCGGATCATTAACAGAGCACTGACATGGCGCAG 254
Qy 152 PheThrTrpArgGluGlyGlnLysGlnLeuPro----- 162
Db 255 -----AAGAGGCTGGCGGACTGTGCTCCAGACCCCAAGGTGGCAGCT 305
Qy 163 ---LeuIleGlyCysValLeuLeuLeuValValSerLeuLeuLeuLeuPhe 181
Db 306 CTCACTGGGAGACCTTCTGACTTCTGACAGCCATCGGGCGGCA----- 350
Qy 182 GlnPheTrpGlnGlyHisThrGlyIleArgTyrLysGlnGlnArgLysSerProLys 201
Db 351 ---TCCTGG----- 356
Qy 202 HisAlaValArgCysAspGlyValValAspCysLysLeuLysSerAspGlu-----Leu 219
Db 357 -----GCCATTGTGGCTGTTCTCTCAGAGTGCACAGAGCGCGCTG 398
Qy 220 GlyCysValArgPheAspTrpAspLysSerLeuLeuLysIleTyrSerGlySerSerHis 239
Db 399 TACCAGTGCAGTCACTCTCTGCGGACGCTCTGCGGCTCATGCTCTTTGACAGAGGAGGG 458
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QY 240 GlnTrpLeuProPheCysSerSerAsnTrpAsnAspSerTyrSerGluLysThrCysGln 259
 DB 459 ACCTGGCGGCTGCTGCTCTCCCTCAGCCAGCGGTAGCGGACTCAGCTGCGAG 518
 QY 260 GlnLeuGlyPheGluSerAlaHisArgThrThrGluValAlaHisArgAsp----- 276
 DB 519 GAGATGGCTTCTCAGGCGACTGACCCACTCGAGCTGCGAGCGGTGCGAACCGCGGCGGC 578
 QY 277 -----PheAlaAsnSerPheSerIleLeuArgTyrAsnSerThrIle 290
 DB 579 AATGGCAGCTCGGGCTTCTCTGTGGACGAGGGAGGCTGCCACACCCAGAGGCTG 638
 QY 291 GlnGluSerLeuHisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSer 310
 DB 639 CTGAGGTCACTCCGCTGTGTGATGATCCCGCAGAGCGGTTCTTGCGCGCCACTCTGCCAA 698
 QY 311 HisCysGlyLeuArgAlaMet-----ThrGlyArgIleValGlyGlyAlaLeuAlaSerAsp 329
 DB 699 GACTGTGGCGCGAGGAGCTGCCCGTGAGCCCGCATCTGTGGAGCGCGGACACCGACTTG 758
 QY 330 SerLysTrpProTrpGlnValSerLeuHisPheGlyThrThrHisIleCysGlyGlyThr 349
 DB 759 GCGCGGTGGCGGTGCGCAAGTCAGCTTGTATGATGGAGCACACTCTGTGGGGATCC 818
 QY 350 LeuIleAspAlaGlnTrpValLeuThrAlaAlaHisCysPhePheValThrArgGluLys 369
 DB 819 CTGCTCTCCGGGAGCTGGGTGCTGACAGCGCGCCACTGC---TTCCCGGAGCGGACCG 875
 QY 370 ValLeuGluGlyTrpLysValTyrAlaGlyThr-----SerAsnLeuHisGlnLeu 386
 DB 876 GTCTCTGCCATGGCGAGGTGGTGGCGGTGGCGTGGCGCCAGCGCTCTCCCGACGGTCTG 935
 QY 387 ProGluAlaAlaSerIleAlaGluIleIleAlaSerAsnTyr----- 401
 DB 936 -----CAGCTGGGGGTGCGAGGTGGTGTCTACACCGGGGCTATCTTCCTTTCCGGAC 989
 QY 402 ---ThrAspGluGluAspTyrAspIleAlaLeuMetArgLeuSerLysProLeuThr 420
 DB 990 CCCAACGAGGAGGAGACAGACGATATTCCTGTGTCACTCTCCAGTCCCTCCGCC 1049
 QY 421 LeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPheSerLeuAsn 440
 DB 1050 CTCACGATATACATCCAGCTGTGTGCTCCAGCTCCGCGCCAGCGCTGTGTGATGGC 1109
 QY 441 GluThrCysTrpIleThrGlyPheGlyThrArgGluThrAspLysThrSerPro 460
 DB 1110 AAGATCTGACCGTGACGGGTGGCGCAACGCGAGTATGCGCCACAGCGCGCGG---1166
 QY 461 PheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAspTyrLeuVal 480
 DB 1167 GTACTCCAGGAGGCTCGAGTCCCATTAATCAGCAATGATGTCTGCAATGGCGTGACTTC 1226
 QY 481 TyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyArgAsp 500
 DB 1227 TATGGAACACGATCAAGCCCAAGATTTCTGTGCTGGCTACCCCGAGGTGGCATTTGAT 1286
 QY 501 SerCysGlnGlyAspSerGlyProLeuValCysGlu-----GlnAsnAsn 516
 DB 1287 GCCTGCCAGGCGGACAGCGGTGGTCCCTTTGTGTGAGGACACCATCTCTCGGACGCCA 1346
 QY 517 ArgTrpTyrLeuAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArgAsnLysPro 536
 DB 1347 CGTGGCGGCTGTGTGGCATTTGATTTGGGCGCACTGGCTGTGGCTGGCGCCAGAGGCCA 1406
 QY 537 GlyValTyrThrLysValThrGluValLeuProTrpIleTyrSerLysMetGluSer 555
 DB 1407 GCGGTCTACACAAAGTCAGTACTTCCGGAGTGGATCTTCAGGCCCATTAAGACT 1463

RESULT 13

; US-09-280-116-22
 ; Sequence 22, Application US/09280116A
 ; Patent No. 6331427
 ; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.
 ; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
 ; FILE REFERENCE: 5800-24, 035800/176965
 ; CURRENT APPLICATION NUMBER: US/09280,116A
 ; CURRENT FILING DATE: 1999-03-26
 ; NUMBER OF SEQ ID NOS: 268
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 22
 ; LENGTH: 610
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: trypsin-like serine proteases
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(610)
 ; OTHER INFORMATION: n = a, t, c, or g
 ; US-09-280-116-22

Alignment Scores:

Pred. No.: 1,25e-24 Length: 610
 Score: 622.50 Matches: 125
 Percent Similarity: 84.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 19
 Query Match: 20.76% Indels: 5
 DB: 4 Gaps: 1

US-09-879-792-12 (1-562) x US-09-280-116-22 (1-610)

QY 299 CysProSerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeuArgAlaMetThr 318
 DB 3 TGCCCTTCCCGAGCGGTATCTCCCTCCAGTGTCCCATCGGACTGAGGGCCATGACC 62
 QY 319 GlyArgIleValGlyGlyAlaLeuAlaSerAspSerLysTrpProTrpGlnValSerLeu 338
 DB 63 GGGCGGATCGTGGAGGGCGCTGCGCTCGCATAGCAAGTGGCTTGGCAAGTGGAGCTG 122
 QY 339 HisPheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGlnTrpValLeuThr 358
 DB 123 CACTTCGGGCACCCACCATCTGTGGAGGCGCGCTCATTTGACGCCCGAGTGGGTGCTAATT 182
 QY 359 AlaAlaHisCysPhePheValThrArgGluLysValLeuGluGlyTyrLysValTyrAla 378
 DB 193 GCGGCGGCTGCTTCTTCTGTCACCGGAGAGGTCTCTGAGGGCTGGAAGTGTACGG 242
 QY 379 GlyThr-SerAsnLeuHis-GlnLeuProGluAlaAlaSerIleAlaGluIleIleAla 398
 DB 243 GGCACCCAGNAACCTGACCCCGCTGCTGAGGCGCTCCATTTGCCGAGATCATCATCA 302
 QY 398 snSerAsnTyrThrAspGluAspAspTyrAspIleAlaLeuMetArgLeuSerLysP 418
 DB 303 ACAGCAATTAACCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 362
 QY 418 toLeu-----ThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyG 435
 DB 363 CCCTTGACCTCTTCCGGTGAGGGAATCTGCACCTCCCGCTCTCTCTGCCCCCGACCCCA 422
 QY 435 InThrPheSerLeuAsnGluThrCys 443
 DB 423 GCACCCCTCTGACGCCCTCGCACCTTGT 448

RESULT 14

; US-09-000-846-1
 ; Sequence 1, Application US/09000846
 ; Patent No. 5981830
 ; GENERAL INFORMATION:
 ; APPLICANT: WU, QINGYU
 ; APPLICANT: SADLER, JASPER
 ; TITLE OF INVENTION: KNOCKOUT MICE AND THEIR PROGENY WITH
 ; TITLE OF INVENTION: DISRUPTED SERINE PROTEASE GENES
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MILLER, WHITE, ZELANO & BRANTIGAN, P.C.

STREET: 2200 CLARENDON BLVD. SUITE 1400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: US
 ZIP: 22201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/000,846
 FILING DATE: 30-DEC-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/866,058
 FILING DATE: 30-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: LEBOVITZ, RICHARD M.
 REGISTRATION NUMBER: 37,067
 REFERENCE/DOCKET NUMBER: BERLX 65P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-243-6333
 TELEFAX: 703-243-6410
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1605 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 35..1282
 US-09-000-846-1

Alignment Scores:
 Pred. No.: 5,26e-24 Length: 1605
 Score: 619.50 Matches: 141
 Percent Similarity: 53.16% Conservative: 61
 Best Local Similarity: 37.11% Mismatches: 133
 Query Match: 20.66% Indels: 45
 DB: 2 Gaps: 12

US-09-879-792-12 (1-562) x US-09-000-846-1 (1-1605)

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Qy 209 ValValAspCysLysLysSerAspGlu-----LeuGlyCysValArgPheAspTrp 226
Db 146 ATGTGACCATCTCTACTGAGAGTACAGAGGACCACTTACCAAGTGCAGCTCAGTCCA 205

Qy 227 AspLysSerLeuLysLysIleTyrSerGlySerHisGlnTrpLeuProIleCysSer 246
Db 206 GGGGACTCAGCGCTTGGCGTGTGTTGACCAAGACGGAGGAACTGCGAGGCTACTGTCTCC 265

Qy 247 SerAsnTrpAsnAspSerTyrSerGluLysThrCysGlnGlnLeuGlyPheGlnSerAla 266
Db 266 TCACGTCCTCAATCCAGGGTGGCAGGGCTCGGCTGTGAGGAGATGGGCTTCTCAGGGCT 325

Qy 267 HisArgThrThrGluValAlaHisArgAspPhe-----AlaAsnSer 280
Db 326 -----CTGGGCGACTCGAGCTGGATGTCGGCACTGCGGCGCCCAACGC 370

Qy 281 PheSer-----IleLeuArgTyrAsnSerThrIleGlnGlu 292
Db 371 ACATCGGGCTCTCTTTGGTGGACGAGGGGCGGACTCCGCTCGCTCAGAGGTGCTGGAT 430

Qy 293 SerLeuHisArgSerGluCysProSerGlnArgTyrIleSerLeuGlnCysSerHisCys 312
Db 431 GTCATCTCTGTATGTGACTCTCTAGAGCCGAGTCTCTGACTGCCACCTGCCAAGACTGT 490

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Qy 313 GlyLeuArgAlaMet---ThrGlyArgIleValGlyGlyAlaLeuAlaSerAspSerLys 331
Db 491 GGGCGAGGAAGCTGCGGGTGGACCGCATTTGGGGGGCCGAGCAGCAGTCTGGGAAGG 550

Qy 332 TrpProTrpGlnValSerLeuHisPheGlyThrHisIleCysGlyGlyThrLeuIle 351
Db 551 TGGCGTGGCAGGTTCAGCTGGCTGATGATGGGACCCACCTCTGTGGGGTCCCTGCTG 610

Qy 352 AspAlaGlnTrpValLeuThrAlaAlaHisCysPhePheValThrArgGluLysValLeu 371
Db 611 TCTGGGAGACTGGGTGCTGACTGCTGCACATTCG---TTTCCAGAGCGGAACCGGGTCTG 667

Qy 372 GluGlyTrpLysValTyrAlaGly-----ThrSerAsnLeuHisGlnLeuPro 387
Db 668 TCTCGGTGGCGAGTATTGCTGTGCTGTAGCCCGGACTCA-----CCC 712

Qy 388 GluAlaAla-----SerIleAlaGluIleIleAlaSerAsnTyr----- 401
Db 713 CATGCTGTGCAACTGGGGGTTCAGGCTGTGATCTATCATGGGGGCTACCTTCCCTTTGGA 772

Qy 402 -----ThrAspGluGluAspAspTyrAspIleAlaLeuMetArgLeuSerLysProLeu 419
Db 773 GACCTTACTATCGACGAAACAGCAATGACATTCCTTGTCTGCACCTCTCTAGCTCCCTG 832

Qy 420 ThrLeuSerAlaHisIleHisProAlaCysLeuProMetHisGlyGlnThrPheSerLeu 439
Db 833 CCTCTCACAGATACATCCAGCCAGTGTGTCTCCTGCTGGGGCAGGCGCTGTGGAT 892

Qy 440 AsnGluThrCysTrpIleThrGlyPheGlyLysThrArgGluThrAspLysThrSer 459
Db 893 GGCAGAGTCTGTACTGTGACCGGCTGGGGTAAACACA---CAGTTCTATGGCCCAACAGGCT 949

Qy 460 ProPheLeuArgGluValGlnValAsnLeuIleAspPheLysLysCysAsnAspTyrLeu 479
Db 950 ATGCTGTCTCCAGAGGCGCGGTTCCCATCATTAAGCAAGCTTTGCCACAGCCCGAC 1009

Qy 480 ValTyrAspSerTyrLeuThrProArgMetMetCysAlaGlyAspLeuArgGlyArg 499
Db 1010 TTCTACGGGAATCAGATCAAGCCCAAGATGTTCTGTGTGCTGCTATCTCTGAGGGTGGCAT 1069

Qy 500 AspSerCysGlnGlyAspSerGlyGlyProLeuValCysGluGlnAsn----- 515
Db 1070 GATCGGTGCCAGGCGCAGTGGAGGCCCTTTGTGTGTGAGACAGCAGCATCTCTGGACA 1129

Qy 516 AsnArgTrpTyrLeuAlaGlyValThrSerTrpGlyThrGlyCysGlyGlnArgAsnLys 535
Db 1130 TCAAGTGGCGGCTATGTGGCATTTGTAAGCTGGGGTACGGGCTGTGCTTTGGCCCGAAG 1189

Qy 536 ProGlyValTyrThrLysValThrGluValLeuProTrpIleTyrSerLysMetGluSer 555
Db 1190 CCAGAGGTGTACCAAGTCACTGACTTCCGGGAGTGGATCTTCAAGGCCATAAGACT 1249

RESULT 15
US-09-820-002-1
; Sequence 1, Application US/09820002
; Patent No. 6482630
; GENERAL INFORMATION:
; APPLICANT: Gan, Weiniu
; APPLICANT: Ye, Jane
; APPLICANT: DiFrancesco, Valentina
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: C1001194
; CURRENT APPLICATION NUMBER: US/09/820,002
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1615
; TYPE: DNA

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ORGANISM: HUMAN

US-09-820-002-1

Alignment Scores:

Pred. No.: 1.29e-23 Length: 1615
Score: 612.00 Matches: 154
Percent Similarity: 45.40% Conservative: 68
Best Local Similarity: 31.43% Mismatches: 169
Query Match: 20.41% Indels: 98
DB: 4 Gaps: 16

US-09-879-792-12 (1-562) x US-09-820-002-1 (1-1615)

QY 95 SerSerGlyArgSerSerSerAlaArgSerAlaSerValThrThrSerProThrArgVal 114
DB 16 TCACACGGAGGGAGGAGACACCCCTGTCA-----ACTGTGGCCCGGGAACTG 66
QY 115 TyrLeuValArgAlaThrProValGlyAlaVal-----ProIleArgSerSerProAla 132
DB 67 GGCCTGGGGAGG---ACATGCTGGGCAATAAATAGTCCCTGGGGGCGAGGAGCT 123
QY 133 ArgSerAlaProAlaThrArgAlaThrArgGluSerProGlyThrSerLeuProLysPhe 152
DB 124 GGCCTGGGGCCAGACCCCTGGCCGCAATGAGGACAGGCTGGCTGTGGC---CCGAGCATG 180
QY 153 ThrTrpArgGluGlyGlnLysGlnLeuPro-----162
DB 181 GTGCTGTGGAGTGGCGGAGCTGTGCCATGCTGCCAGACCACCAAGGTGGCAGCTCTC 240
QY 163 LeuIleGlyCysValLeuLeuLeuLeuAlaLeuValSerLeuIleLeuPheGln 182
DB 241 ACTGGGGGACCTGTCTACTCTTGACAGCCATCGGGGGCGCA-----282
QY 183 PheTrpGlnGlyHisThrGlyIleArgTyrLysGluGlnArgGluSerCysProLysHis 202
DB 283 TCCTGG-----288
QY 203 AlaValArgCysAspGlyValValAspCysLysLysLeuLysSerAspGlu-----LeuGly 220
DB 289 -----GCCATTGTGGCTGTCTCTCTCAGGAGTGACCGAGGCGCGCTGTAC 333
QY 221 CysValArgPheAspTrpAspLysSerLeuLeuLysIleTyrSerGlySerHisGln 240
DB 334 CAGTGCAGTCACTGCTGGAGCGCTCGCTCATGCTTTTGACAGAGGAGGAGGAG 393
QY 241 TrpLeuProIleCysSerSerAsnTrpAsnAspSerTyrSerGluLysThrCysGlnGln 260
DB 394 TGGCGGCTGCTGTGCTCTCTCGCTCCACCGCGGTAGCGGAGCTCAGCTGCGAGGAG 453
QY 261 LeuGlyPheGluSerAlaHisArgThrThrGluValAlaHisArgAspPheAlaHisSer 280
DB 454 ATGGGCTTC-----462
QY 281 PheSerIleLeuArgTyrAsnSerThrIleGlnGluSerLeuHisArgSerGluCysPro 300
DB 463 -----CTCAGTGATTGCCCC 477
QY 301 SerGlnArgTyrIleSerLeuGlnCysSerHisCysGlyLeuArgAlaMet---ThrGly 319
DB 478 AGAGGCGGTTCGTGGCCGCATCTGCCAAGACTGTGGCCGAGGAGGAGTGGCCGTGGAC 537
QY 320 ArgIleValGlyGlyAlaLeuAlaSerAspSerLysTrpProTrpGlnValSerLeuHis 339
DB 538 CGCATCTGGGAGGCGGGGACACAGCTTGGGCGGTGGCCCTGGCAAGTCAAGCTTGGC 597
QY 340 PheGlyThrThrHisIleCysGlyGlyThrLeuIleAspAlaGlnTrpValLeuThrAla 359
DB 598 TATGATGACACACACTCTGTGGGGATCCCTCTCCGGGGAGCTGGGTGTGTGACAGCC 657
QY 360 AlaHisCysPhePheValThrArgGluLysValLeuGluGlyTyrLysValTyrAlaGly 379
DB 658 GCCCACTGC---TTCCCGGAGCGGAGACCGGGTCTCTGTCGGATGGCGAGTGTTCGGGT 714

QY 380 Thr-----SerAsnLeuHisGlnLeuProGluAlaAlaSerIleAlaGluIleIle 396
DB 715 GCGGTGGCCAGGCGCTCTCCCAAGGCTCTG-----CAGCTGGGGTGCAGGCTGTGGTC 768
QY 397 IleAsnSerAsnTyr-----ThrAspGluGluAspAspTyrAspIle 410
DB 769 TACCACGGGGGCTATCTTCCTTTTCGGGACCCCAACAGAGGAGGAGACAGCAATATT 828
QY 411 AlaLeuMetArgLeuSerLysProLeuThrLeuSerAlaHisIleHisProAlaCysLeu 430
DB 829 GGCCTGGTCCACTCTCCAGTCCCTCCCTCCACAAATACATCCAGCTGTGTGCTCTC 888
QY 431 ProMetHisGlyGlnThrPheSerLeuAsnGluThrCysTrpIleThrGlyPheGlyLys 450
DB 889 CCAGCTGCCGCGCCAGGCGCTGGTGGATGCAAGATCTGTACCGTGACGGCTGGGGCAAC 948
QY 451 ThrArgGluThrAspAspLysThrSerProPheLeuArgGluValGlnValAsnLeuIle 470
DB 949 ACAGCTACTATGCGCAACAGGCGCGG---GTACTCCAGAGGCTCGAGTCCCAATATC 1005
QY 471 AspPheLysLysCysAsnAspTyrLeuValTyrAspSerTyrLeuThrProArgMet 490
DB 1006 AGCAATGATCTCTGCATGCGCGTCTTCTATGGAACCCAGATCAAGCCCAAGATGTT 1065
QY 491 CysAlaGlyAspLeuArgGlyGlyArgAspSerCysGlnGlyAspSerGlyGlyProLeu 510
DB 1066 TGTCTGCTACCCCGAGGCTGGCATTTGATCCCTGCCAGGCGGACAGCGGTGTCTCTTT 1125
QY 511 ValCysGlu-----GlnAsnAsnAspTyrTyrLeuAlaGlyValThrSerTrp 526
DB 1126 GTGTGTGAGGACAGCATCTCTCGACCGCCACGTTGGCGCTGTGTGCGCATTTGAGTTGG 1185
QY 527 GlyThrGlyCysGlyGlnArgAsnLysProGlyValTyrThrLysValThrGluValLeu 546
DB 1186 GGCATGGCTGTGCTGCGCCAGAGGCGCTTACACCAAGTCAAGTCAAGTCAAGTCAAGT 1245
QY 547 ProTrpIleTyrSerLysMetGluSer 555
DB 1246 GAGTGGATCTTCCAGGCGCATAAAGACT 1272

Search completed: December 17, 2003, 21:55:35
Job time : 138 secs